ERROR DETECTED   SUGGESTED   CORRECTION

SERIAL NUMBER: 09/672,725

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 ✓ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

```
        RAW SEQUENCE LISTING              DATE: 10/06/2000
        PATENT APPLICATION:  US/09/672,725   TIME: 12:46:04

        Input Set : A:\485402_1.txt
        Output Set: N:\CRF3\10062000\I672725.raw
```

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     4 <110> APPLICANT: Stocker, Penny J.
     5         Steimel-Crespi, Dorothy T.
     6         Crespi, Charles L.
     7         Rief, Timothy C
     8         Patten, Christopher J.
    10 <120> TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
    13 <130> FILE REFERENCE: G0307/7017
C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/672,725
C--> 15 <141> CURRENT FILING DATE: 2000-09-28
    15 <150> PRIOR APPLICATION NUMBER: US 60/156,510
    16 <151> PRIOR FILING DATE: 1999-09-28
    18 <160> NUMBER OF SEQ ID NOS: 32
    20 <170> SOFTWARE: FastSEQ for Windows Version 3.0


ERRORED SEQUENCES

    22 <210> SEQ ID NO: 1
    23 <211> LENGTH: 4279
    24 <212> TYPE: DNA
    25 <213> ORGANISM: Canis familiaris
    27 <220> FEATURE:
    28 <221> NAME/KEY: CDS
    29 <222> LOCATION: (17)...(3859)
    31 <400> SEQUENCE: 1
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    33                     Met Asp Pro Glu Gly Gly Arg Lys Gly Ser Ala Glu
    34                       1           5                  10
    36  aag aac ttc tgg aaa atg ggc aaa aaa agt aaa aaa aat gag aag aaa   100
    37  Lys Asn Phe Trp Lys Met Gly Lys Lys Ser Lys Lys Asn Glu Lys Lys
    38          15                  20                  25
    40  gaa aag aaa cca act gtc agc acg ttt gca atg ttt cgc tat tca aat   148
    41  Glu Lys Lys Pro Thr Val Ser Thr Phe Ala Met Phe Arg Tyr Ser Asn
    42      30                  35                  40
    44  tgg ctt gat agg ttg tat atg ttg gtg ggg aca atg gct gcc atc atc   196
    45  Trp Leu Asp Arg Leu Tyr Met Leu Val Gly Thr Met Ala Ala Ile Ile
    46   45              50                  55                  60
    48  cat gga gct gca ctc cct ctc atg atg ctg gtt ttt gga aac atg aca   244
    49  His Gly Ala Ala Leu Pro Leu Met Met Leu Val Phe Gly Asn Met Thr
    50              65                  70                  75
    52  gat agc ttt,gca aat gca gga att tca aga aac aaa act ttt cca gtt   292
    53  Asp Ser Phe Ala Asn Ala Gly Ile Ser Arg Asn Lys Thr Phe Pro Val
    54              80                  85                  90
    56  ata att aat gaa agt att acg aac aat aca caa cat ttc atc aac cat   340
    57  Ile Ile Asn Glu Ser Ile Thr Asn Asn Thr Gln His Phe Ile Asn His
    58          95                  100                 105
    60  ctg gag gag gaa atg acc acg tat gcc tat tat tac agt ggg atc ggt   388
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RAW SEQUENCE LISTING   DATE: 10/06/2000
PATENT APPLICATION: US/09/672,725   TIME: 12:46:04

Input Set : A:\485402_1.txt
Output Set: N:\CRF3\10062000\I672725.raw

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61  Leu Glu Glu Glu Met Thr Thr Tyr Ala Tyr Tyr Tyr Ser Gly Ile Gly
62      110                 115                 120
64  gct ggc gtg ctg gtg gct gct tac atc cag gtt tca ttc tgg tgc ctg      436
65  Ala Gly Val Leu Val Ala Ala Tyr Ile Gln Val Ser Phe Trp Cys Leu
66  125                 130                 135                 140
68  gca gca gga aga cag ata ctc aaa att aga aaa caa ttt ttt cat gct      484
69  Ala Ala Gly Arg Gln Ile Leu Lys Ile Arg Lys Gln Phe Phe His Ala
70              145                 150                 155
72  atc atg cga cag gag att ggc tgg ttt gac gtg cat gac gtt ggg gag      532
73  Ile Met Arg Gln Glu Ile Gly Trp Phe Asp Val His Asp Val Gly Glu
74              160                 165                 170
76  ctt aac acc cgg ctc aca gac gat gtc tcc aaa atc aat gaa gga att      580
77  Leu Asn Thr Arg Leu Thr Asp Asp Val Ser Lys Ile Asn Glu Gly Ile
78              175                 180                 185
80  ggc gac aaa att gga atg ttc ttt cac tca ata gca aca ttt ttc acc      628
81  Gly Asp Lys Ile Gly Met Phe Phe His Ser Ile Ala Thr Phe Phe Thr
82      190                 195                 200
84  ggt ttt ata gtg ggg ttt aca cgt ggt tgg aag cta acc ctt gtg att      676
85  Gly Phe Ile Val Gly Phe Thr Arg Gly Trp Lys Leu Thr Leu Val Ile
86  205                 210                 215                 220
88  ttg gcc atc agc cct gtt ctt gga ctt tca gcc gcc atc tgg gca aag      724
89  Leu Ala Ile Ser Pro Val Leu Gly Leu Ser Ala Ala Ile Trp Ala Lys
90              225                 230                 235
92  ata cta tct tca ttt act gat aaa gaa ctc ttg gcc tat gca aaa gct      772
93  Ile Leu Ser Ser Phe Thr Asp Lys Glu Leu Leu Ala Tyr Ala Lys Ala
94              240                 245                 250
96  gga gca gta gct gaa gaa gtc tta gca gca atc aga act gtg att gcc      820
97  Gly Ala Val Ala Glu Glu Val Leu Ala Ala Ile Arg Thr Val Ile Ala
98          255                 260                 265
100 ttt gga gga caa aag aaa gaa ctt gaa agg tac aac aaa aat tta gaa      868
101 Phe Gly Gly Gln Lys Lys Glu Leu Glu Arg Tyr Asn Lys Asn Leu Glu
102     270                 275                 280
104 gaa gct aaa gga att ggg ata aag aaa gct atc acg gcc aac att tct      916
105 Glu Ala Lys Gly Ile Gly Ile Lys Lys Ala Ile Thr Ala Asn Ile Ser
106 285                 290                 295                 300
108 att ggt gcc gct ttc tta ttg atc tat gca tca tat gct ctg gct ttc      964
109 Ile Gly Ala Ala Phe Leu Leu Ile Tyr Ala Ser Tyr Ala Leu Ala Phe
110             305                 310                 315
112 tgg tat ggg acc tcc ttg gtc ctc tcc agt gaa tat tct att gga caa      1012
113 Trp Tyr Gly Thr Ser Leu Val Leu Ser Ser Glu Tyr Ser Ile Gly Gln
114             320                 325                 330
116 gta ctc act gtc ttc ttt tct gta tta att ggg gct ttt agt att gga      1060
117 Val Leu Thr Val Phe Phe Ser Val Leu Ile Gly Ala Phe Ser Ile Gly
118             335                 340                 345
120 cag gca tcc cca agc att gaa gca ttt gca aac gca aga gga gca gct      1108
121 Gln Ala Ser Pro Ser Ile Glu Ala Phe Ala Asn Ala Arg Gly Ala Ala
122     350                 355                 360
124 tat gaa atc ttc aag ata att gac aat aaa cca agc att gac agc tat      1156
125 Tyr Glu Ile Phe Lys Ile Ile Asp Asn Lys Pro Ser Ile Asp Ser Tyr
```

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126  365                    370                 375                    380
128  tcg aag agt gga cat aaa cca gat aat att aag gga aat ttg gaa ttc      1204
.129  Ser Lys Ser Gly His Lys Pro Asp Asn Ile Lys Gly Asn Leu Glu Phe
130                   385                 390                    395
132  aaa aat gtt cac ttc agt tac cct tct cga aaa gaa gtt aag atc tta      1252
133  Lys Asn Val His Phe Ser Tyr Pro Ser Arg Lys Glu Val Lys Ile Leu
134                   400                 405                 410
136  aag ggt ctc aac ctg aag gtt cag agt ggg cag aca gtg gcg ctg gtt      1300
137  Lys Gly Leu Asn Leu Lys Val Gln Ser Gly Gln Thr Val Ala Leu Val
138              415                 420                    425
140  ggg aac agt ggc tgc ggg aag agc acg acc gtg cag ctg atg cag agg      1348
141  Gly Asn Ser Gly Cys Gly Lys Ser Thr Thr Val Gln Leu Met Gln Arg
142         430                 435                    440
144  ctc tat gac ccc aca gat ggc atg gtc tgt att gat gga cag gac att      1396
145  Leu Tyr Asp Pro Thr Asp Gly Met Val Cys Ile Asp Gly Gln Asp Ile
146  445                 450                 455                 460
148  agg acc ata aat gta agg cat ctt cgg gaa att act ggt gtg gtg agt      1444
149  Arg Thr Ile Asn Val Arg His Leu Arg Glu Ile Thr Gly Val Val Ser
150                   465                 470                 475
152  cag gag cct gtg ttg ttt gcc acc acg ata gct gaa aac att cgc tat      1492
153  Gln Glu Pro Val Leu Phe Ala Thr Thr Ile Ala Glu Asn Ile Arg Tyr
154              480                 485                    490
156  ggc cgc gaa aat gtc acc atg gat gag att gag aaa gct gtt aag gaa      1540
157  Gly Arg Glu Asn Val Thr Met Asp Glu Ile Glu Lys Ala Val Lys Glu
158         495                 500                    505
160  gcc aat gcc tat gat ttt atc atg aaa cta cct aat aaa ttt gac act      1588
161  Ala Asn Ala Tyr Asp Phe Ile Met Lys Leu Pro Asn Lys Phe Asp Thr
162         510                 515                 520
164  ctg gtt gga gag aga ggg gcc cag ctg agt ggt gga cag aaa cag aga      1636
165  Leu Val Gly Glu Arg Gly Ala Gln Leu Ser Gly Gly Gln Lys Gln Arg
166  525                 530                 535                    540
168  atc gcc att gct cgg gcc ctg gtt cgc aac ccc aag att ctt ctg ctg      1684
169  Ile Ala Ile Ala Arg Ala Leu Val Arg Asn Pro Lys Ile Leu Leu Leu
170                   545                 550                    555
172  gat gag gca acg tca gct ctg gac act gaa agt gaa gca gtg gtt cag      1732
173  Asp Glu Ala Thr Ser Ala Leu Asp Thr Glu Ser Glu Ala Val Val Gln
174              560                 565                    570
176  gtg gcc ctg gat aag gcc aga aaa ggc cgg act acc att gtg ata gct      1780
177  Val Ala Leu Asp Lys Ala Arg Lys Gly Arg Thr Thr Ile Val Ile Ala
178         575                 580                    585
180  cat cgt ttg tct aca gtt cgt aat gcc gat gtc att gct ggt ttt gat      1828
181  His Arg Leu Ser Thr Val Arg Asn Ala Asp Val Ile Ala Gly Phe Asp
182         590                 595                 600
184  gat gga gtc att gtg gag aaa gga aat cat gat gaa ctc atg aaa gag      1876
185  Asp Gly Val Ile Val Glu Lys Gly Asn His Asp Glu Leu Met Lys Glu
186  605                 610                 615                    620
188  aag ggc att tac ttc aaa ctt gtc aca atg cag aca aga gga aat gaa      1924
189  Lys Gly Ile Tyr Phe Lys Leu Val Thr Met Gln Thr Arg Gly Asn Glu
190              625                 630                    635
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RAW SEQUENCE LISTING   DATE: 10/06/2000
PATENT APPLICATION: US/09/672,725   TIME: 12:46:04

Input Set : A:\485402_1.txt
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192  att gag tta gaa aat gcc act ggt gaa tcc aaa agt gaa agt gat gcc      1972
193  Ile Glu Leu Glu Asn Ala Thr Gly Glu Ser Lys Ser Glu Ser Asp Ala
194          640                 645                 650
196  ttg gaa atg tct cca aaa gat tca ggg tcc agt tta ata aaa aga aga      2020
197  Leu Glu Met Ser Pro Lys Asp Ser Gly Ser Ser Leu Ile Lys Arg Arg
198          655                 660                 665
200  tca act cgc agg agt ata cat gca cca caa ggc caa gac aga aag ctt      2068
201  Ser Thr Arg Arg Ser Ile His Ala Pro Gln Gly Gln Asp Arg Lys Leu
202          670                 675                 680
204  ggt aca aaa gag gac ttg aat gag aat gta cct cca gtt tcc ttc tgg      2116
205  Gly Thr Lys Glu Asp Leu Asn Glu Asn Val Pro Pro Val Ser Phe Trp
206  685                 690                 695                 700
208  agg att ctg aag ctg aac tca act gaa tgg cct tat ttt gtg gtt ggt      2164
209  Arg Ile Leu Lys Leu Asn Ser Thr Glu Trp Pro Tyr Phe Val Val Gly
210          705                 710                 715
212  ata ttt tgt gct att ata aac gga ggc ctg caa cca gca ttt tca ata      2212
213  Ile Phe Cys Ala Ile Ile Asn Gly Gly Leu Gln Pro Ala Phe Ser Ile
214          720                 725                 730
216  ata ttt tca agg att ata ggg atc ttt acc cga gat gag gat cct gaa      2260
217  Ile Phe Ser Arg Ile Ile Gly Ile Phe Thr Arg Asp Glu Asp Pro Glu
218          735                 740                 745
220  aca aaa cga cag aat agt aac atg ttt tct gta ttg ttt cta gtc ctt      2308
221  Thr Lys Arg Gln Asn Ser Asn Met Phe Ser Val Leu Phe Leu Val Leu
222          750                 755                 760
224  gga att att tct ttt att aca ttt ttc ctc cag ggc ttc aca ttt ggc      2356
225  Gly Ile Ile Ser Phe Ile Thr Phe Phe Leu Gln Gly Phe Thr Phe Gly
226  765                 770                 775                 780
228  aaa gct ggg gag atc ctc act aag cgg ctt cga tac atg gtt ttc aga      2404
229  Lys Ala Gly Glu Ile Leu Thr Lys Arg Leu Arg Tyr Met Val Phe Arg
230                  785                 790                 795
232  tcc atg ctg aga cag gat gtc agc tgg ttt gat gac cct aaa aac acc      2452
233  Ser Met Leu Arg Gln Asp Val Ser Trp Phe Asp Asp Pro Lys Asn Thr
234                  800                 805                 810
236  act gga gca ttg aca acc agg ctt gcc aat gat gcg gct caa gtt aaa      2500
237  Thr Gly Ala Leu Thr Thr Arg Leu Ala Asn Asp Ala Ala Gln Val Lys
238          815                 820                 825
240  ggg gct ata ggt tcc agg ctt gct gtc att acc cag aat ata gca aat      2548
241  Gly Ala Ile Gly Ser Arg Leu Ala Val Ile Thr Gln Asn Ile Ala Asn
242          830                 835                 840
244  ctt ggg aca ggc att att ata tcc tta atc tat ggt tgg caa tta aca      2596
245  Leu Gly Thr Gly Ile Ile Ile Ser Leu Ile Tyr Gly Trp Gln Leu Thr
246  845                 850                 855                 860
248  ctt tta ctc tta gca att gta ccc atc att gca ata gca gga gtt gtt      2644
249  Leu Leu Leu Leu Ala Ile Val Pro Ile Ile Ala Ile Ala Gly Val Val
250                  865                 870                 875
252  gaa atg aaa atg ttg tct gga caa gca ctg aaa gat aag aaa gag cta      2692
253  Glu Met Lys Met Leu Ser Gly Gln Ala Leu Lys Asp Lys Lys Glu Leu
254                  880                 885                 890
256  gaa gga gct ggg aag att gct aca gaa gcc atc gaa aac ttc cga act      2740
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257  Glu Gly Ala Gly Lys Ile Ala Thr Glu Ala Ile Glu Asn Phe Arg Thr
258          895                     900                 905
260  gtt gtt tct ttg act cgg gag cag aag ttt gaa tac atg tat gca cag      2788
261  Val Val Ser Leu Thr Arg Glu Gln Lys Phe Glu Tyr Met Tyr Ala Gln
262          910                     915                 920
264  agt ttg caa gta cca tac aga aac tct ttg agg aaa gca cac atc ttc      2836
265  Ser Leu Gln Val Pro Tyr Arg Asn Ser Leu Arg Lys Ala His Ile Phe
266      925                     930                 935             940
268  ggg gtc tca ttt tct atc acc cag gca atg atg tat ttt tcc tat gct      2884
269  Gly Val Ser Phe Ser Ile Thr Gln Ala Met Met Tyr Phe Ser Tyr Ala
270                      945                 950                 955
272  ggc tgt ttc cgg ttt ggt gcc tac ttg gtg gca aat gag ttc atg aac      2932
273  Gly Cys Phe Arg Phe Gly Ala Tyr Leu Val Ala Asn Glu Phe Met Asn
274              960                 965                 970
276  ttt cag gat gtt ctt ttg gta ttc tca gct att gtc ttt ggt gcc atg      2980
277  Phe Gln Asp Val Leu Leu Val Phe Ser Ala Ile Val Phe Gly Ala Met
278          975                     980                 985
280  gca gtg ggg cag gtc agt tca ttt gct cct gac tat gcc aaa gcc aaa      3028
281  Ala Val Gly Gln Val Ser Ser Phe Ala Pro Asp Tyr Ala Lys Ala Lys
282      990                     995                 1000
284  gta tca gca gcc cac gtc atc atg atc att gaa aaa agc cct ctg att      3076
285  Val Ser Ala Ala His Val Ile Met Ile Ile Glu Lys Ser Pro Leu Ile
286  1005                    1010                1015                1020
288  gac agc tac agc cct cac ggc ctc aag cca aat acg ttg gaa gga aat      3124
289  Asp Ser Tyr Ser Pro His Gly Leu Lys Pro Asn Thr Leu Glu Gly Asn
290                  1025                    1030                1035
292  gtg aca ttt aat gag gtc gtg ttc aac tat ccc act cga cca gac atc      3172
293  Val Thr Phe Asn Glu Val Val Phe Asn Tyr Pro Thr Arg Pro Asp Ile
294              1040                    1045                1050
296  ccc gtg ctc cag ggg ctg agc ctc gag gtg aag aag ggc cag acg ctg      3220
297  Pro Val Leu Gln Gly Leu Ser Leu Glu Val Lys Lys Gly Gln Thr Leu
298          1055                    1060                1065
300  gcc ctc gta ggt agc agt ggc tgt ggg aag agc aca gtt gtt cag ctc      3268
301  Ala Leu Val Gly Ser Ser Gly Cys Gly Lys Ser Thr Val Val Gln Leu
302      1070                    1075                1080
304  cta gag cgc ttc tat gac ccc ttg gct ggt tca gtg cta att gat ggc      3316
305  Leu Glu Arg Phe Tyr Asp Pro Leu Ala Gly Ser Val Leu Ile Asp Gly
306  1085                    1090                1095                1100
308  aaa gag ata aag cac ctg aat gtc cag tgg ctc cga gca cac ctg ggc      3364
309  Lys Glu Ile Lys His Leu Asn Val Gln Trp Leu Arg Ala His Leu Gly
310              1105                    1110                1115
312  atc gtg tct cag gag ccc atc ctg ttt gac tgc agc att gcc gag aac      3412
313  Ile Val Ser Gln Glu Pro Ile Leu Phe Asp Cys Ser Ile Ala Glu Asn
314              1120                    1125                1130
316  att gcc tat gga gac aac agc cgg gtc gta tca cat gaa gag att atg      3460
317  Ile Ala Tyr Gly Asp Asn Ser Arg Val Val Ser His Glu Glu Ile Met
318          1135                    1140                1145
320  cag gca gcc aag gag gcc aac ata cac cac ttc atc gag aca ctc cct      3508
321  Gln Ala Ala Lys Glu Ala Asn Ile His His Phe Ile Glu Thr Leu Pro
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322     1150              1155              1160
324  gag aaa tac aac acc aga gta gga gac aaa gga acc cag ctc tct ggt    3556
325  Glu Lys Tyr Asn Thr Arg Val Gly Asp Lys Gly Thr Gln Leu Ser Gly
326  1165              1170              1175              1180
328  ggc cag aaa cag cgc att gcc ata gct cgc gct ctt gtt aga cag cct    3604
329  Gly Gln Lys Gln Arg Ile Ala Ile Ala Arg Ala Leu Val Arg Gln Pro
330              1185              1190              1195
332  cat att ttg ctt ttg gat gaa gct aca tca gct ctg gat aca gaa agt    3652
333  His Ile Leu Leu Leu Asp Glu Ala Thr Ser Ala Leu Asp Thr Glu Ser
334              1200              1205              1210
336  gaa aag gtt gtc caa gaa gcc ctg gac aaa gcc aga gaa ggc cgc acc    3700
337  Glu Lys Val Val Gln Glu Ala Leu Asp Lys Ala Arg Glu Gly Arg Thr
338          1215              1220              1225
340  tgc att gtg atc gcc cac cgc ttg tcc acc atc cag aat gca gat tta    3748
341  Cys Ile Val Ile Ala His Arg Leu Ser Thr Ile Gln Asn Ala Asp Leu
342      1230              1235              1240
344  ata gtg gtg ttt cag aat ggc aaa gtc aag gag cat ggc aca cat caa    3796
345  Ile Val Val Phe Gln Asn Gly Lys Val Lys Glu His Gly Thr His Gln
346  1245              1250              1255              1260
348  cag ctg ctg gcc cag aaa ggc atc tat ttt tcc atg gtc agt gtc cag    3844
349  Gln Leu Leu Ala Gln Lys Gly Ile Tyr Phe Ser Met Val Ser Val Gln
350              1265              1270              1275
352  gct gga gca aag cgc tagtgaactg tggccatatg agctgttaaa tattttttaa    3899
353  Ala Gly Ala Lys Arg
354              1280
356  tatttgtgtt aaaacatggc atttaatcaa agttaaaagg tgagcactta ctggaaaaac    3959
357  tatgtagaac tacctgttta acatttcttg ctgcaactga agatcattcc accagttca     4019
358  gagtcttcag attttataat taaaggaacc aaaagaaaca ttatctgatg gaataaaata    4079
359  ctggtgttaa ttgcattata aaattataga gtaattcaaa gtagattttg ttaataaatt    4139
360  gtataatttt tgtttatatt ttatttgtaa cttactgctt tgctgaaaga ttatagaagt    4199
361  ggtaaaaagt actgaatgtt tgaataaagt gctagctata ataaaactaa actttttatat   4259
E--> 362  caaaaaaaaa aaaaaaaaaa                                             4279
364  <210> SEQ ID NO: 2
365  <211> LENGTH: 1281
366  <212> TYPE: PRT
367  <213> ORGANISM: Canis familiaris
369  <400> SEQUENCE: 2
370  Met Asp Pro Glu Gly Gly Arg Lys Gly Ser Ala Glu Lys Asn Phe Trp
371  1               5                   10                  15
372  Lys Met Gly Lys Lys Ser Lys Lys Asn Glu Lys Lys Glu Lys Lys Pro
373              20                  25                  30
374  Thr Val Ser Thr Phe Ala Met Phe Arg Tyr Ser Asn Trp Leu Asp Arg
375          35                  40                  45
376  Leu Tyr Met Leu Val Gly Thr Met Ala Ala Ile Ile His Gly Ala Ala
377      50                  55                  60
378  Leu Pro Leu Met Met Leu Val Phe Gly Asn Met Thr Asp Ser Phe Ala
379  65                  70                  75                  80
380  Asn Ala Gly Ile Ser Arg Asn Lys Thr Phe Pro Val Ile Ile Asn Glu
381              85                  90                  95
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<handwritten>
4279 End of line nucleic acid number missing. All lines must have numbering.

Computer program only counts 4259. This causes an error between the number listed, <211> 4279 and number found: 4259.
</handwritten>

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382  Ser Ile Thr Asn Asn Thr Gln His Phe Ile Asn His Leu Glu Glu Glu
383              100              105              110
384  Met Thr Thr Tyr Ala Tyr Tyr Ser Gly Ile Gly Ala Gly Val Leu
385          115              120              125
386  Val Ala Ala Tyr Ile Gln Val Ser Phe Trp Cys Leu Ala Ala Gly Arg
387          130              135              140
388  Gln Ile Leu Lys Ile Arg Lys Gln Phe Phe His Ala Ile Met Arg Gln
389  145              150              155              160
390  Glu Ile Gly Trp Phe Asp Val His Asp.Val Gly Glu Leu Asn Thr Arg
391              165              170              175
392  Leu Thr Asp Asp Val Ser Lys Ile Asn Glu Gly Ile Gly Asp Lys Ile
393              180              185              190
394  Gly Met Phe Phe His Ser Ile Ala Thr Phe Phe Thr Gly Phe Ile Val
395          195              200              205
396  Gly Phe Thr Arg Gly Trp Lys Leu Thr Leu Val Ile Leu Ala Ile Ser
397          210              215              220
398  Pro Val Leu Gly Leu Ser Ala Ala Ile Trp Ala Lys Ile Leu Ser Ser
399  225              230              235              240
400  Phe Thr Asp Lys Glu Leu Leu Ala Tyr Ala Lys Ala Gly Ala Val Ala
401              245              250              255
402  Glu Glu Val Leu Ala Ala Ile Arg Thr Val Ile Ala Phe Gly Gly Gln
403              260              265              270
404  Lys Lys Glu Leu Glu Arg Tyr Asn Lys Asn Leu Glu Glu Ala Lys Gly
405          275              280              285
406  Ile Gly Ile Lys Lys Ala Ile Thr Ala Asn Ile Ser Ile Gly Ala Ala
407          290              295              300
408  Phe Leu Leu Ile Tyr Ala Ser Tyr Ala Leu Ala Phe Trp Tyr Gly Thr
409  305              310              315              320
410  Ser Leu Val Leu Ser Ser Glu Tyr Ser Ile Gly Gln Val Leu Thr Val
411              325              330              335
412  Phe Phe Ser Val Leu Ile Gly Ala Phe Ser Ile Gly Gln Ala Ser Pro
413              340              345              350
414  Ser Ile Glu Ala Phe Ala Asn Ala Arg Gly Ala Ala Tyr Glu Ile Phe
415          355              360              365
416  Lys Ile Ile Asp Asn Lys Pro Ser Ile Asp Ser Tyr Ser Lys Ser Gly
417          370              375              380
418  His Lys Pro Asp Asn Ile Lys Gly Asn Leu Glu Phe Lys Asn Val His
419  385              390              395              400
420  Phe Ser Tyr Pro Ser Arg Lys Glu Val Lys Ile Leu Lys Gly Leu Asn
421              405              410              415
422  Leu Lys Val Gln Ser Gly Gln Thr Val Ala Leu Val Gly Asn Ser Gly
423              420              425              430
424  Cys Gly Lys Ser Thr Thr Val Gln Leu Met Gln Arg Leu Tyr Asp Pro
425          435              440              445
426  Thr Asp Gly Met Val Cys Ile Asp Gly Gln Asp Ile Arg Thr Ile Asn
427          450              455              460
428  Val Arg His Leu Arg Glu Ile Thr Gly Val Val Ser Gln Glu Pro Val
429  465              470              475              480
430  Leu Phe Ala Thr Thr Ile Ala Glu Asn Ile Arg Tyr Gly Arg Glu Asn
```

```
431                 485              490              495
432 Val Thr Met Asp Glu Ile Glu Lys Ala Val Lys Glu Ala Asn Ala Tyr
433             500              505              510
434 Asp Phe Ile Met Lys Leu Pro Asn Lys Phe Asp Thr Leu Val Gly Glu
435         515              520              525
436 Arg Gly Ala Gln Leu Ser Gly Gly Gln Lys Gln Arg Ile Ala Ile Ala
437     530              535              540
438 Arg Ala Leu Val Arg Asn Pro Lys Ile Leu Leu Leu Asp Glu Ala Thr
439 545              550              555              560
440 Ser Ala Leu Asp Thr Glu Ser Glu Ala Val Gln Val Ala Leu Asp
441             565              570              575
442 Lys Ala Arg Lys Gly Arg Thr Thr Ile Val Ile Ala His Arg Leu Ser
443             580              585              590
444 Thr Val Arg Asn Ala Asp Val Ile Ala Gly Phe Asp Asp Gly Val Ile
445         595              600              605
446 Val Glu Lys Gly Asn His Asp Glu Leu Met Lys Glu Lys Gly Ile Tyr
447     610              615              620
448 Phe Lys Leu Val Thr Met Gln Thr Arg Gly Asn Glu Ile Glu Leu Glu
449 625              630              635              640
450 Asn Ala Thr Gly Glu Ser Lys Ser Glu Ser Asp Ala Leu Glu Met Ser
451             645              650              655
452 Pro Lys Asp Ser Gly Ser Ser Leu Ile Lys Arg Arg Ser Thr Arg Arg
453             660              665              670
454 Ser Ile His Ala Pro Gln Gly Gln Asp Arg Lys Leu Gly Thr Lys Glu
455         675              680              685
456 Asp Leu Asn Glu Asn Val Pro Pro Val Ser Phe Trp Arg Ile Leu Lys
457     690              695              700
458 Leu Asn Ser Thr Glu Trp Pro Tyr Phe Val Val Gly Ile Phe Cys Ala
459 705              710              715              720
460 Ile Ile Asn Gly Gly Leu Gln Pro Ala Phe Ser Ile Ile Phe Ser Arg
461             725              730              735
462 Ile Ile Gly Ile Phe Thr Arg Asp Glu Asp Pro Glu Thr Lys Arg Gln
463             740              745              750
464 Asn Ser Asn Met Phe Ser Val Leu Phe Leu Val Leu Gly Ile Ile Ser
465         755              760              765
466 Phe Ile Thr Phe Phe Leu Gln Gly Phe Thr Phe Gly Lys Ala Gly Glu
467     770              775              780
468 Ile Leu Thr Lys Arg Leu Arg Tyr Met Val Phe Arg Ser Met Leu Arg
469 785              790              795              800
470 Gln Asp Val Ser Trp Phe Asp Asp Pro Lys Asn Thr Thr Gly Ala Leu
471             805              810              815
472 Thr Thr Arg Leu Ala Asn Asp Ala Ala Gln Val Lys Gly Ala Ile Gly
473             820              825              830
474 Ser Arg Leu Ala Val Ile Thr Gln Asn Ile Ala Asn Leu Gly Thr Gly
475         835              840              845
476 Ile Ile Ile Ser Leu Ile Tyr Gly Trp Gln Leu Thr Leu Leu Leu Leu
477     850              855              860
478 Ala Ile Val Pro Ile Ile Ala Ile Ala Gly Val Val Glu Met Lys Met
479 865              870              875              880
```

```
              RAW SEQUENCE LISTING              DATE: 10/06/2000
              PATENT APPLICATION:  US/09/672,725  TIME: 12:46:04

              Input Set : A:\485402_1.txt
              Output Set: N:\CRF3\10062000\I672725.raw

       480  Leu Ser Gly Gln Ala Leu Lys Asp Lys Lys Glu Leu Glu Gly Ala Gly
       481            885                     890                     895
       482  Lys Ile Ala Thr Glu Ala Ile Glu Asn Phe Arg Thr Val Val Ser Leu
       483            900                     905                     910
       484  Thr Arg Glu Gln Lys Phe Glu Tyr Met Tyr Ala Gln Ser Leu Gln Val
       485            915                     920                     925
       486  Pro Tyr Arg Asn Ser Leu Arg Lys Ala His Ile Phe Gly Val Ser Phe
       487        930                 935                 940
       488  Ser Ile Thr Gln Ala Met Met Tyr Phe Ser Tyr Ala Gly Cys Phe Arg
       489  945                 950                 955                 960
       490  Phe Gly Ala Tyr Leu Val Ala Asn Glu Phe Met Asn Phe Gln Asp Val
       491            965                     970                     975
       492  Leu Leu Val Phe Ser Ala Ile Val Phe Gly Ala Met Ala Val Gly Gln
       493            980                     985                     990
       494  Val Ser Ser Phe Ala Pro Asp Tyr Ala Lys Ala Lys Val Ser Ala Ala
       495        995                 1000                1005
       496  His Val Ile Met Ile Ile Glu Lys Ser Pro Leu Ile Asp Ser Tyr Ser
       497        1010                1015                1020
       498  Pro His Gly Leu Lys Pro Asn Thr Leu Glu Gly Asn Val Thr Phe Asn
E-->   499  1025            .        1030                1035            104
       500  Glu Val Val Phe Asn Tyr Pro Thr Arg Pro Asp Ile Pro Val Leu Gln
       501                1045                1050                1055
       502  Gly Leu Ser Leu Glu Val Lys Lys Gly Gln Thr Leu Ala Leu Val Gly
       503            1060                1065                1070
       504  Ser Ser Gly Cys Gly Lys Ser Thr Val Val Gln Leu Leu Glu Arg Phe
       505        1075                1080                1085
       506  Tyr Asp Pro Leu Ala Gly Ser Val Leu Ile Asp Gly Lys Glu Ile Lys
       507        1090                1095                1100
       508  His Leu Asn Val Gln Trp Leu Arg Ala His Leu Gly Ile Val Ser Gln
       509  1105                1110                1115                1120
       510  Glu Pro Ile Leu Phe Asp Cys Ser Ile Ala Glu Asn Ile Ala Tyr Gly
       511            1125                1130                1135
       512  Asp Asn Ser Arg Val Val Ser His Glu Glu Ile Met Gln Ala Ala Lys
       513            1140                1145                1150
       514  Glu Ala Asn Ile His His Phe Ile Glu Thr Leu Pro Glu Lys Tyr Asn
       515        1155                1160                1165
       516  Thr Arg Val Gly Asp Lys Gly Thr Gln Leu Ser Gly Gly Gln Lys Gln
       517        1170                1175                1180
       518  Arg Ile Ala Ile Ala Arg Ala Leu Val Arg Gln Pro His Ile Leu Leu
       519  1185                1190                1195                1200
       520  Leu Asp Glu Ala Thr Ser Ala Leu Asp Thr Glu Ser Glu Lys Val Val
       521            1205                1210                1215
       522  Gln Glu Ala Leu Asp Lys Ala Arg Glu Gly Arg Thr Cys Ile Val Ile
       523            1220                1225                1230
       524  Ala His Arg Leu Ser Thr Ile Gln Asn Ala Asp Leu Ile Val Val Phe
       525        1235                1240                1245
       526  Gln Asn Gly Lys Val Lys Glu His Gly Thr His Gln Gln Leu Leu Ala
       527        1250                1255                1260
       528  Gln Lys Gly Ile Tyr Phe Ser Met Val Ser Val Gln Ala Gly Ala Lys
```

Invalid amino acid number.

Asn 1040

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/672,725

DATE: 10/06/2000
TIME: 12:46:04

Input Set : A:\485402_1.txt
Output Set: N:\CRF3\10062000\I672725.raw

```
529  1265              1270              1275              1280
530  Arg
533  <210> SEQ ID NO: 3
534  <211> LENGTH: 4317
535  <212> TYPE: DNA
536  <213> ORGANISM: Canis familiaris
538  <220> FEATURE:
539  <221> NAME/KEY: CDS
540  <222> LOCATION: (70)...(3912)
542  <400> SEQUENCE: 3
543  ctaagtcgga gtatcttctt cccaaattcc cttctcggtg gaggttgcga aggaaagccc      60
544  gaggtgacg atg gat cct gaa gga ggc cgt aag ggg agt gca gag aag aac     111
545           Met Asp Pro Glu Gly Gly Arg Lys Gly Ser Ala Glu Lys Asn
546            1               5                    10
548  ttc tgg aaa atg ggc aaa aaa agt aaa aaa gag aag aaa gaa aag aaa      159
549  Phe Trp Lys Met Gly Lys Lys Ser Lys Lys Glu Lys Lys Glu Lys Lys
550  15               20                   25                   30
552  cca act gtc agc acg ttt gca atg ttt cgc tat tca aat tgg ctt gat     207
553  Pro Thr Val Ser Thr Phe Ala Met Phe Arg Tyr Ser Asn Trp Leu Asp
554                   35                   40                   45
556  agg ttg tat atg ttg gtg ggg aca atg gct gcc atc atc cat gga gct     255
557  Arg Leu Tyr Met Leu Val Gly Thr Met Ala Ala Ile Ile His Gly Ala
558           50                   55                   60
560  gca ctc cct ctc atg atg ctg gtt ttt gga aac atg aca gat agc ttt     303
561  Ala Leu Pro Leu Met Met Leu Val Phe Gly Asn Met Thr Asp Ser Phe
562           65                   70                   75
564  gca aat gca gga att tca aga aac aaa act ttt cca gtt ata att aat     351
565  Ala Asn Ala Gly Ile Ser Arg Asn Lys Thr Phe Pro Val Ile Ile Asn
566       80                   85                   90
568  gaa agt att acg aac aat aca caa cat ttc atc aac cat ctg gag gag     399
569  Glu Ser Ile Thr Asn Asn Thr Gln His Phe Ile Asn His Leu Glu Glu
570  95                   100                  105                  110
572  gaa atg acc acg tat gcc tat tat tac agt ggg atc ggt gct ggc gtg     447
573  Glu Met Thr Thr Tyr Ala Tyr Tyr Tyr Ser Gly Ile Gly Ala Gly Val
574                   115                  120                  125
576  ctg gtg gct gct tac atc cag gtt tca ttc tgg tgc ctg gca gca gga     495
577  Leu Val Ala Ala Tyr Ile Gln Val Ser Phe Trp Cys Leu Ala Ala Gly
578                   130                  135                  140
580  aga cag ata ctc aaa att aga aaa caa ttt ttt cat gct atc atg cga     543
581  Arg Gln Ile Leu Lys Ile Arg Lys Gln Phe Phe His Ala Ile Met Arg
582           145                  150                  155
584  cag gag att ggc tgg ttt gac gtg cat gac gtt ggg gag ctt aac acc     591
585  Gln Glu Ile Gly Trp Phe Asp Val His Asp Val Gly Glu Leu Asn Thr
586      160                  165                  170
588  cgg ctc aca gac gat gtc tcc aaa atc aat gaa gga att ggc gac aaa     639
589  Arg Leu Thr Asp Asp Val Ser Lys Ile Asn Glu Gly Ile Gly Asp Lys
590  175                  180                  185                  190
592  gtt gga atg ttc ttt caa tca ata gca aca ttt ttc acc ggt ttt ata     687
593  Val Gly Met Phe Phe Gln Ser Ile Ala Thr Phe Phe Thr Gly Phe Ile
```

RAW SEQUENCE LISTING   DATE: 10/06/2000
PATENT APPLICATION: US/09/672,725   TIME: 12:46:04

Input Set : A:\485402_1.txt
Output Set: N:\CRF3\10062000\I672725.raw

```
594                195              200              205
596  gtg ggg ttt aca cct ggt tgg aag cta acc ctt gtg att ttg gcc atc      735
597  Val Gly Phe Thr Pro Gly Trp Lys Leu Thr Leu Val Ile Leu Ala Ile
598              210              215              220
600  agc cct gtt ctt gga ctt tca gcc gcc atc tgg gca aag ata cta tct      783
601  Ser Pro Val Leu Gly Leu Ser Ala Ala Ile Trp Ala Lys Ile Leu Ser
602              225              230              235
604  tca ttt act gat aaa gaa ctc ttg gcc tat gca aaa gct gga gca gta      831
605  Ser Phe Thr Asp Lys Glu Leu Leu Ala Tyr Ala Lys Ala Gly Ala Val
606              240              245              250
608  gct gaa gaa gtc tta gca gca atc aga act gtg att gcc ttt gga gga      879
609  Ala Glu Glu Val Leu Ala Ala Ile Arg Thr Val Ile Ala Phe Gly Gly
610  255              260              265              270
612  caa aag aaa gaa ctt gaa agg tac aac aaa aat tta gaa gaa gct aaa      927
613  Gln Lys Lys Glu Leu Glu Arg Tyr Asn Lys Asn Leu Glu Glu Ala Lys
614              275              280              285
616  aga att ggg ata aag aaa gct atc acg gcc aac att tct att ggt gcc      975
617  Arg Ile Gly Ile Lys Lys Ala Ile Thr Ala Asn Ile Ser Ile Gly Ala
618              290              295              300
620  gct ttc tta ttg atc tat gca tca tat gct ctg gct ttc tgg tat ggg     1023
621  Ala Phe Leu Leu Ile Tyr Ala Ser Tyr Ala Leu Ala Phe Trp Tyr Gly
622              305              310              315
624  acc tcc ttg gtc ctc tcc agt gaa tat act att gga cag gta ctc act     1071
625  Thr Ser Leu Val Leu Ser Ser Glu Tyr Thr Ile Gly Gln Val Leu Thr
626  320              325              330
628  gtc ttc ttt tct gta tta att ggg gct ttt agt att gga cag gca tcc     1119
629  Val Phe Phe Ser Val Leu Ile Gly Ala Phe Ser Ile Gly Gln Ala Ser
630  335              340              345              350
632  cca agc att gaa gca ttt gca aac gca aga gga gca gct tat gaa atc     1167
633  Pro Ser Ile Glu Ala Phe Ala Asn Ala Arg Gly Ala Ala Tyr Glu Ile
634              355              360              365
636  ttc aag ata att gac aat aaa cca agc att gac agc tat tcg aag agt     1215
637  Phe Lys Ile Ile Asp Asn Lys Pro Ser Ile Asp Ser Tyr Ser Lys Ser
638              370              375              380
640  gga cat aaa cca gat aat att aag gga aat ttg gaa ttc aaa aat gtt     1263
641  Gly His Lys Pro Asp Asn Ile Lys Gly Asn Leu Glu Phe Lys Asn Val
642              385              390              395
644  cac ttc agt tac cct tct cga aaa gaa gtt aag atc tta aag ggt ctc     1311
645  His Phe Ser Tyr Pro Ser Arg Lys Glu Val Lys Ile Leu Lys Gly Leu
646              400              405              410
648  aac ctg aag gtt cag agt ggg cag aca gtg gcg ctg gtt ggg aac agt     1359
649  Asn Leu Lys Val Gln Ser Gly Gln Thr Val Ala Leu Val Gly Asn Ser
650  415              420              425              430
652  ggc tgc ggg aag agc acg acc gtg cag ctg atg cag agg ctc tat gac     1407
653  Gly Cys Gly Lys Ser Thr Thr Val Gln Leu Met Gln Arg Leu Tyr Asp
654              435              440              445
656  ccc aca gat ggc atg gtc tgt att gat gga cag gac att agg acc ata     1455
657  Pro Thr Asp Gly Met Val Cys Ile Asp Gly Gln Asp Ile Arg Thr Ile
658              450              455              460
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RAW SEQUENCE LISTING   DATE: 10/06/2000
PATENT APPLICATION: US/09/672,725   TIME: 12:46:04

Input Set : A:\485402_1.txt
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```
660  aat gta agg cat ctt cgg gaa att act ggt gtg gtg agt cag gag cct    1503
661  Asn Val Arg His Leu Arg Glu Ile Thr Gly Val Val Ser Gln Glu Pro
662          465                 470                 475
664  gtg ttg ttt gcc acc acg ata gct gaa aac att cgc tat ggc cgc gaa    1551
665  Val Leu Phe Ala Thr Thr Ile Ala Glu Asn Ile Arg Tyr Gly Arg Glu
666          480                 485                 490
668  aat gtc acc atg gat gag att gag aaa gct gtt aag gaa gcc aat gcc    1599
669  Asn Val Thr Met Asp Glu Ile Glu Lys Ala Val Lys Glu Ala Asn Ala
670  495                 500                 505                 510
672  tat gat ttt atc atg aaa cta cct aat aaa ttt gac act ctg gtt gga    1647
673  Tyr Asp Phe Ile Met Lys Leu Pro Asn Lys Phe Asp Thr Leu Val Gly
674              515                 520                 525
676  gag aga ggg gcc cgg ctg agt ggt gga cag aaa cag aga atc gcc att    1695
677  Glu Arg Gly Ala Arg Leu Ser Gly Gly Gln Lys Gln Arg Ile Ala Ile
678              530                 535                 540
680  gct cgg gcc ctg gtt cgc aac ccc aag att ctt ctg ctg gat gag gca    1743
681  Ala Arg Ala Leu Val Arg Asn Pro Lys Ile Leu Leu Leu Asp Glu Ala
682          545                 550                 555
684  acg tca gct ctg gac act gaa agt gaa gca gtg gtt cag gtg gcc ctg    1791
685  Thr Ser Ala Leu Asp Thr Glu Ser Glu Ala Val Val Gln Val Ala Leu
686          560                 565                 570
688  gat aag gcc aga aaa ggc cgg act acc att gtg ata gct cat cgt ttg    1839
689  Asp Lys Ala Arg Lys Gly Arg Thr Thr Ile Val Ile Ala His Arg Leu
690  575                 580                 585                 590
692  tct aca gtt cgt aat gcc gat gtc att gct ggt ttt gat gat gga gtc    1887
693  Ser Thr Val Arg Asn Ala Asp Val Ile Ala Gly Phe Asp Asp Gly Val
694              595                 600                 605
696  att gtg gag aaa gga aat cat gat gaa ctc atg aaa gag aag ggc att    1935
697  Ile Val Glu Lys Gly Asn His Asp Glu Leu Met Lys Glu Lys Gly Ile
698              610                 615                 620
700  tac ttc aaa ctt gtc aca atg cag aca aga gga aat gaa att gag tta    1983
701  Tyr Phe Lys Leu Val Thr Met Gln Thr Arg Gly Asn Glu Ile Glu Leu
702          625                 630                 635
704  gaa aat gcc act ggt gaa tcc aaa agt gaa agt gat gcc ttg gaa atg    2031
705  Glu Asn Ala Thr Gly Glu Ser Lys Ser Glu Ser Asp Ala Leu Glu Met
706          640                 645                 650
708  tct cca aaa gat tca ggg tcc agt tta ata aaa aga aga tca act cgc    2079
709  Ser Pro Lys Asp Ser Gly Ser Ser Leu Ile Lys Arg Arg Ser Thr Arg
710  655                 660                 665                 670
712  agg agt ata cat gca cca caa ggc caa gac aga aag ctt ggt aca aaa    2127
713  Arg Ser Ile His Ala Pro Gln Gly Gln Asp Arg Lys Leu Gly Thr Lys
714              675                 680                 685
716  gag gac ttg aat gag aat gtt cct tca gtt tcc ttc tgg agg att ctg    2175
717  Glu Asp Leu Asn Glu Asn Val Pro Ser Val Ser Phe Trp Arg Ile Leu
718              690                 695                 700
720  aag ctg aac tca act gaa tgg cct tat ttt gtg gtt ggt ata ttt tgt    2223
721  Lys Leu Asn Ser Thr Glu Trp Pro Tyr Phe Val Val Gly Ile Phe Cys
722          705                 710                 715
724  gct att ata aac gga ggc ctg caa cca gca ttt tca ata ata ttt tca    2271
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725  Ala Ile Ile Asn Gly Gly Leu Gln Pro Ala Phe Ser Ile Ile Phe Ser
726      720               725               730
728  agg att ata ggg atc ttt acc cga gat gag gat cct gaa aca aaa cga    2319
729  Arg Ile Ile Gly Ile Phe Thr Arg Asp Glu Asp Pro Glu Thr Lys Arg
730  735           740               745               750
732  cag aat agt aac atg ttt tct gta ttg ttt cta gtc ctt gga att att    2367
733  Gln Asn Ser Asn Met Phe Ser Val Leu Phe Leu Val Leu Gly Ile Ile
734          755               760               765
736  tct ttt att aca ttt ttc ctc cag ggc ttc aca ttt ggc aaa gct ggg    2415
737  Ser Phe Ile Thr Phe Phe Leu Gln Gly Phe Thr Phe Gly Lys Ala Gly
738          770               775               780
740  gag atc ctc act aag cgg ctt cga tac atg gtt ttc aga tcc atg ctg    2463
741  Glu Ile Leu Thr Lys Arg Leu Arg Tyr Met Val Phe Arg Ser Met Leu
742          785               790               795
744  aga cag gat gtc agc tgg ttt gat gac cct aaa aac acc act gga gca    2511
745  Arg Gln Asp Val Ser Trp Phe Asp Asp Pro Lys Asn Thr Thr Gly Ala
746      800               805               810
748  ttg aca acc agg ctt gcc aat gat gcg gct caa gtt aaa ggg gct ata    2559
749  Leu Thr Thr Arg Leu Ala Asn Asp Ala Ala Gln Val Lys Gly Ala Ile
750  815               820               825               830
752  ggt tcc agg ctt gct gtc att acc cag aat ata gca aat ctt ggg aca    2607
753  Gly Ser Arg Leu Ala Val Ile Thr Gln Asn Ile Ala Asn Leu Gly Thr
754          835               840               845
756  ggc att att ata tcc tta atc tat ggt tgg caa tta aca ctt tta ctc    2655
757  Gly Ile Ile Ile Ser Leu Ile Tyr Gly Trp Gln Leu Thr Leu Leu Leu
758          850               855               860
760  tta gca att gta ccc atc att gca ata gca gga gtt gtt gaa atg aaa    2703
761  Leu Ala Ile Val Pro Ile Ile Ala Ile Ala Gly Val Val Glu Met Lys
762          865               870               875
764  atg ttg tct gga caa gca ctg aaa gat aag aaa gag cta gaa gga gct    2751
765  Met Leu Ser Gly Gln Ala Leu Lys Asp Lys Lys Glu Leu Glu Gly Ala
766      880               885               890
768  ggg aag att gct aca gaa gcc atc gaa aac ttc cga act gtt gtt tct    2799
769  Gly Lys Ile Ala Thr Glu Ala Ile Glu Asn Phe Arg Thr Val Val Ser
770  895               900               905               910
772  ttg act cgg gag cag aag ttt gaa tac atg tat gca cag agt ttg caa    2847
773  Leu Thr Arg Glu Gln Lys Phe Glu Tyr Met Tyr Ala Gln Ser Leu Gln
774          915               920               925
776  gta cca tac aga aac tct ttg agg aaa gca cac atc ttc ggg gtc tca    2895
777  Val Pro Tyr Arg Asn Ser Leu Arg Lys Ala His Ile Phe Gly Val Ser
778          930               935               940
780  ttt tct atc acc cag gca atg atg tat ttt tcc tat gct ggc tgt ttc    2943
781  Phe Ser Ile Thr Gln Ala Met Met Tyr Phe Ser Tyr Ala Gly Cys Phe
782          945               950               955
784  cgg ttt ggt gcc tac ttg gtg gca aat gag ttc atg aac ttt cag gat    2991
785  Arg Phe Gly Ala Tyr Leu Val Ala Asn Glu Phe Met Asn Phe Gln Asp
786      960               965               970
788  gtt ctt ttg gta ttc tca gct att gtc ttt ggt gcc atg gca gtg ggg    3039
789  Val Leu Leu Val Phe Ser Ala Ile Val Phe Gly Ala Met Ala Val Gly
```

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790   975              980              985              990
792   cag gtc agt tca ttt gct cct gac tat gcc aaa gcc aaa gta tca gca     3087
793   Gln Val Ser Ser Phe Ala Pro Asp Tyr Ala Lys Ala Lys Val Ser Ala
794                   995              1000             1005
796   gcc cac gtc atc atg atc att gaa aaa agc cct ctg att gac agc tac     3135
797   Ala His Val Ile Met Ile Ile Glu Lys Ser Pro Leu Ile Asp Ser Tyr
798              1010             1015             1020
800   agc cct cac ggc ctc aag cca aat acg ttg gaa gga aat gtg aca ttt     3183
801   Ser Pro His Gly Leu Lys Pro Asn Thr Leu Glu Gly Asn Val Thr Phe
802         1025             1030             1035
804   aat gag gtc gtg ttc aac tat ccc act cga cca gac atc ccc gtg ctc     3231
805   Asn Glu Val Val Phe Asn Tyr Pro Thr Arg Pro Asp Ile Pro Val Leu
806      1040           . 1045             1050
808   cag ggg ctg agc ctc gag gtg aag aag ggc cag acg ctg gcc ctc gta     3279
809   Gln Gly Leu Ser Leu Glu Val Lys Lys Gly Gln Thr Leu Ala Leu Val
810   1055             1060             1065             1070
812   ggt agc agt ggc tgt ggg aag agc aca gtt gtt cag ctc cta gag cgc     3327
813   Gly Ser Ser Gly Cys Gly Lys Ser Thr Val Val Gln Leu Leu Glu Arg
814              1075             1080             1085
816   ttc tat gac ccc ttg gct ggt tca gtg cta att gat ggc aaa gag ata     3375
817   Phe Tyr Asp Pro Leu Ala Gly Ser Val Leu Ile Asp Gly Lys Glu Ile
818              1090             1095             1100
820   aag cac ctg aat gtc cag tgg ctc cga gca cac ctg ggc atc gtg tct     3423
821   Lys His Leu Asn Val Gln Trp Leu Arg Ala His Leu Gly Ile Val Ser
822         1105             1110             1115
824   cag gag ccc atc ctg ttt gac tgc agc att gcc gag aac att gcc tat     3471
825   Gln Glu Pro Ile Leu Phe Asp Cys Ser Ile Ala Glu Asn Ile Ala Tyr
826   1120             1125             1130
828   gga gac aac agc cgg gtc gta tca cat gaa gag att atg cag gca gcc     3519
829   Gly Asp Asn Ser Arg Val Val Ser His Glu Glu Ile Met Gln Ala Ala
830   1135             1140             1145             1150
832   aag gag gcc aac ata cac cac ttc atc gag aca ctc cct gag aaa tac     3567
833   Lys Glu Ala Asn Ile His His Phe Ile Glu Thr Leu Pro Glu Lys Tyr
834              1155             1160             1165
836   aac acc aga gta gga gac aaa gga acc cag ctc tct ggt ggc cag aaa     3615
837   Asn Thr Arg Val Gly Asp Lys Gly Thr Gln Leu Ser Gly Gly Gln Lys
838         1170             1175             1180
840   cag cgc att gcc atá gct cgc gct ctt gtt aga cag cct cat att ttg     3663
841   Gln Arg Ile Ala Ile Ala Arg Ala Leu Val Arg Gln Pro His Ile Leu
842      1185             1190             1195
844   ctt ttg gat gaa gct aca tca gct ctg gat aca gaa agt gaa aag gtt     3711
845   Leu Leu Asp Glu Ala Thr Ser Ala Leu Asp Thr Glu Ser Glu Lys Val
846   1200             1205             1210
848   gtc caa gaa gcc ctg gac aaa gcc aga gaa ggc cgc acc tgc att gtg     3759
849   Val Gln Glu Ala Leu Asp Lys Ala Arg Glu Gly Arg Thr Cys Ile Val
850   1215 ·           1220             1225             1230
852   atc gcc cac cgc ttg tcc acc atc cag aat gca gat tta ata gtg gtg     3807
853   Ile Ala His Arg Leu Ser Thr Ile Gln Asn Ala Asp Leu Ile Val Val
854              1235             1240             1245
```

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856  ttt cag aat ggc aaa gtc aag gag cat ggc aca cat caa cag ctg ctg        3855
857  Phe Gln Asn Gly Lys Val Lys Glu His Gly Thr His Gln Gln Leu Leu
858          1250                1255                1260
860  gct cag aaa ggc atc tat ttt tcc atg atc agt gtc cag gct gga gca        3903
861  Ala Gln Lys Gly Ile Tyr Phe Ser Met Ile Ser Val Gln Ala Gly Ala
862          1265                1270                1275
864  aag cgc tag tgaactgtgg ccatgtgagc tgttaaatat tttttaatat             3952
865  Lys Arg
866      1280
868  ttgtgttaaa acatggcatt taatcaaagt taaaaggtga gcacttactg gaaaaactat    4012
869  gtagaactac ctgtttaaca tttcttgctg caactgaaga tcattccacc aagttcagag    4072
870  tcttcagatt ttataattaa aggaaccaaa agaaacatta tctgatggaa taaaatattg    4132
871  gtgttaattg cattataaaa ttatagagta attcaaagta gattttgtta ataaattgta    4192
872  taattttgt ttatatttta tttgtaactt actgctttgc tgaaagatta tagaagtggt    4252
873  aaaaagtact gaatgtttga ataaagtgct agctataata aaactaaact tttatatgaa    43̶1̶3̶
E-->  874  aaaaa
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4317

Invalid end of line numbering. refer to p. 6

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1641 <210> SEQ ID NO: 22
1642 <211> LENGTH: 4279
1643 <212> TYPE: DNA
1644 <213> ORGANISM: Canis familiaris
1646 <220> FEATURE:
1647 <221> NAME/KEY: CDS
1648 <222> LOCATION: (17)...(3859)
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1652                Met Asp Pro Glu Gly Gly Arg Lys Gly Ser Ala Glu
1653                 1           5                10
1655 aag aac ttc tgg aaa atg ggc aaa aaa agt aaa aaa aat gag aag aaa        100
1656 Lys Asn Phe Trp Lys Met Gly Lys Lys Ser Lys Lys Asn Glu Lys Lys
1657         15              20              25
1659 gaa aag aaa cca act gtc agc acg ttt gca atg ttt cgc tat tca aat        148
1660 Glu Lys Lys Pro Thr Val Ser Thr Phe Ala Met Phe Arg Tyr Ser Asn
1661         30              35              40
1663 tgg ctt gat agg ttg tat atg ttg gtg ggg aca atg gct gcc atc atc        196
1664 Trp Leu Asp Arg Leu Tyr Met Leu Val Gly Thr Met Ala Ala Ile Ile
1665 45              50              55              60
1667 cat gga gct gca ctc cct ctc atg atg ctg gtt ttt gga aac atg aca        244
1668 His Gly Ala Ala Leu Pro Leu Met Met Leu Val Phe Gly Asn Met Thr
1669             65              70              75
1671 gat agc ttt gca aat gca gga att tca aga aac aaa act ttt cca gtt        292
1672 Asp Ser Phe Ala Asn Ala Gly Ile Ser Arg Asn Lys Thr Phe Pro Val
1673         80              85              90
1675 ata att aat gaa agt att acg aac aat aca caa cat ttc atc aac cat        340
1676 Ile Ile Asn Glu Ser Ile Thr Asn Asn Thr Gln His Phe Ile Asn His
1677         95              100             105
1679 ctg gag gag gaa atg acc acg tat gcc tat tat tac agt ggg atc ggt        388
1680 Leu Glu Glu Glu Met Thr Thr Tyr Ala Tyr Tyr Tyr Ser Gly Ile Gly
1681     110             115             120
1683 gct ggc gtg ctg gtg gct gct tac atc cag gtt tca ttc tgg tgc ctg        436
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1684    Ala Gly Val Leu Val Ala Ala Tyr Ile Gln Val Ser Phe Trp Cys Leu
1685    125                 130                 135                 140
1687    gca gca gga aga cag ata ctc aaa att aga aaa caa ttt ttt cat gct        484
1688    Ala Ala Gly Arg Gln Ile Leu Lys Ile Arg Lys Gln Phe Phe His Ala
1689                    145                 150                 155
1691    atc atg cga cag gag att ggc tgg ttt gac gtg cat gac gtt ggg gag        532
1692    Ile Met Arg Gln Glu Ile Gly Trp Phe Asp Val His Asp Val Gly Glu
1693                    160                 165                 170
1695    ctt aac acc cgg ctc aca gac gat gtc tcc aaa atc aat gaa gga att        580
1696    Leu Asn Thr Arg Leu Thr Asp Asp Val Ser Lys Ile Asn Glu Gly Ile
1697                    175                 180                 185
1699    ggc gac aaa att gga atg ttt ttt caa tca ata gca aca ttt ttc acc        628
1700    Gly Asp Lys Ile Gly Met Phe Phe Gln Ser Ile Ala Thr Phe Phe Thr
1701            190                 195                 200
1703    ggt ttt ata gtg ggg ttt aca cgt ggt tgg aag cta acc ctt gtg att        676
1704    Gly Phe Ile Val Gly Phe Thr Arg Gly Trp Lys Leu Thr Leu Val Ile
1705    205                 210                 215                 220
1707    ttg gcc atc agc cct gtt ctt gga ctt tca gcc gcc atc tgg gca aag        724
1708    Leu Ala Ile Ser Pro Val Leu Gly Leu Ser Ala Ala Ile Trp Ala Lys
1709                    225                 230                 235
1711    ata cta tct tca ttt act gat aaa gaa ctc ttg gcc tat gca aaa gct        772
1712    Ile Leu Ser Ser Phe Thr Asp Lys Glu Leu Leu Ala Tyr Ala Lys Ala
1713                    240                 245                 250
1715    gga gca gta gct gaa gaa gtc tta gca gca atc aga act gtg att gcc        820
1716    Gly Ala Val Ala Glu Glu Val Leu Ala Ala Ile Arg Thr Val Ile Ala
1717            255                 260                 265
1719    ttt gga gga caa aag aaa gaa ctt gaa agg tac aac aaa aat tta gaa        868
1720    Phe Gly Gly Gln Lys Lys Glu Leu Glu Arg Tyr Asn Lys Asn Leu Glu
1721            270                 275                 280
1723    gaa gct aaa gga att ggg ata aag aaa gct atc acg gcc aac att tct        916
1724    Glu Ala Lys Gly Ile Gly Ile Lys Lys Ala Ile Thr Ala Asn Ile Ser
1725    285                 290                 295                 300
1727    att ggt gcc gct ttc tta ttg atc tat gca tca tat gct ctg gct ttc        964
1728    Ile Gly Ala Ala Phe Leu Leu Ile Tyr Ala Ser Tyr Ala Leu Ala Phe
1729                    305                 310                 315
1731    tgg tat ggg acc tcc ttg gtc ctc tcc agt gaa tat tct att gga caa        1012
1732    Trp Tyr Gly Thr Ser Leu Val Leu Ser Ser Glu Tyr Ser Ile Gly Gln
1733                    320                 325                 330
1735    gta ctc act gtc ttc ttt tct gta tta att ggg gct ttt agt att gga        1060
1736    Val Leu Thr Val Phe Phe Ser Val Leu Ile Gly Ala Phe Ser Ile Gly
1737            335                 340                 345
1739    cag gca tcc cca agc att gaa gca ttt gca aac gca aga gga gca gct        1108
1740    Gln Ala Ser Pro Ser Ile Glu Ala Phe Ala Asn Ala Arg Gly Ala Ala
1741            350                 355                 360
1743    tat gaa atc ttc aag ata att gac aat aaa cca agc att gac agc tat        1156
1744    Tyr Glu Ile Phe Lys Ile Ile Asp Asn Lys Pro Ser Ile Asp Ser Tyr
1745    365                 370                 375                 380
1747    tcg aag agt gga cat aaa cca gat aat att aag gga aat ttg gaa ttc        1204
1748    Ser Lys Ser Gly His Lys Pro Asp Asn Ile Lys Gly Asn Leu Glu Phe
```

```
1749                  385                 390                 395
1751  aaa aat gtt cac ttc agt tac cct tct cga aaa gaa gtt aag atc tta    1252
1752  Lys Asn Val His Phe Ser Tyr Pro Ser Arg Lys Glu Val Lys Ile Leu
1753                  400                 405                 410
1755  aag ggt ctc aac ctg aag gtt cag agt ggg cag aca gtg gcg ctg gtt    1300
1756  Lys Gly Leu Asn Leu Lys Val Gln Ser Gly Gln Thr Val Ala Leu Val
1757                  415                 420                 425
1759  ggg aac agt ggc tgc ggg aag agc acg acc gtg cag ctg atg cag agg    1348
1760  Gly Asn Ser Gly Cys Gly Lys Ser Thr Thr Val Gln Leu Met Gln Arg
1761            430                 435                 440
1763  ctc tat gac ccc aca gat ggc atg gtc tgt att gat gga cag gac att    1396
1764  Leu Tyr Asp Pro Thr Asp Gly Met Val Cys Ile Asp Gly Gln Asp Ile
1765  445                 450                 455                 460
1767  agg acc ata aat gta agg cat ctt cgg gaa att act ggt gtg gtg agt    1444
1768  Arg Thr Ile Asn Val Arg His Leu Arg Glu Ile Thr Gly Val Val Ser
1769                  465                 470                 475
1771  cag gag cct gtg ttg ttt gcc acc acg ata gct gaa aac att cgc tat    1492
1772  Gln Glu Pro Val Leu Phe Ala Thr Thr Ile Ala Glu Asn Ile Arg Tyr
1773                  480                 485                 490
1775  ggc cgc gaa aat gtc acc atg gat gag att gag aaa gct gtt aag gaa    1540
1776  Gly Arg Glu Asn Val Thr Met Asp Glu Ile Glu Lys Ala Val Lys Glu
1777            495                 500                 505
1779  gcc aat gcc tat gat ttt atc atg aaa cta cct aat aaa ttt gac act    1588
1780  Ala Asn Ala Tyr Asp Phe Ile Met Lys Leu Pro Asn Lys Phe Asp Thr
1781        510                 515                 520
1783  ctg gtt gga gag aga ggg gcc cag ctg agt ggt gga cag aaa cag aga    1636
1784  Leu Val Gly Glu Arg Gly Ala Gln Leu Ser Gly Gly Gln Lys Gln Arg
1785  525                 530                 535                 540
1787  atc gcc att gct cgg gcc ctg gtt cgc aac ccc aag att ctt ctg ctg    1684
1788  Ile Ala Ile Ala Arg Ala Leu Val Arg Asn Pro Lys Ile Leu Leu Leu
1789                  545                 550                 555
1791  gat gag gca acg tca gct ctg gac act gaa agt gaa gca gtg gtt cag    1732
1792  Asp Glu Ala Thr Ser Ala Leu Asp Thr Glu Ser Glu Ala Val Val Gln
1793                  560                 565                 570
1795  gtg gcc ctg gat aag gcc aga aaa ggc cgg act acc att gtg ata gct    1780
1796  Val Ala Leu Asp Lys Ala Arg Lys Gly Arg Thr Thr Ile Val Ile Ala
1797            575                 580                 585
1799  cat cgt ttg tct aca gtt cgt aat gcc gat gtc att gct ggt ttt gat    1828
1800  His Arg Leu Ser Thr Val Arg Asn Ala Asp Val Ile Ala Gly Phe Asp
1801        590                 595                 600
1803  gat gga gtc att gtg gag aaa gga aat cat gat gaa ctc atg aaa gag    1876
1804  Asp Gly Val Ile Val Glu Lys Gly Asn His Asp Glu Leu Met Lys Glu
1805  605                 610                 615                 620
1807  aag ggc att tac ttc aaa ctt gtc aca atg cag aca aga gga aat gaa    1924
1808  Lys Gly Ile Tyr Phe Lys Leu Val Thr Met Gln Thr Arg Gly Asn Glu
1809                  625                 630                 635
1811  att gag tta gaa aat gcc act ggt gaa tcc aaa agt gaa agt gat gcc    1972
1812  Ile Glu Leu Glu Asn Ala Thr Gly Glu Ser Lys Ser Glu Ser Asp Ala
1813                  640                 645                 650
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RAW SEQUENCE LISTING   DATE: 10/06/2000
PATENT APPLICATION: US/09/672,725   TIME: 12:46:04

Input Set : A:\485402_1.txt
Output Set: N:\CRF3\10062000\I672725.raw

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1815  ttg gaa atg tct cca aaa gat tca ggg tcc agt tta ata aaa aga aga    2020
1816  Leu Glu Met Ser Pro Lys Asp Ser Gly Ser Ser Leu Ile Lys Arg Arg
1817          655                 660                 665
1819  tca act cgc agg agt ata cat gca cca caa ggc caa gac aga aag ctt    2068
1820  Ser Thr Arg Arg Ser Ile His Ala Pro Gln Gly Gln Asp Arg Lys Leu
1821          670                 675                 680
1823  ggt aca aaa gag gac ttg aat gag aat gta cct cca gtt tcc ttc tgg    2116
1824  Gly Thr Lys Glu Asp Leu Asn Glu Asn Val Pro Pro Val Ser Phe Trp
1825  685                 690                 695                 700
1827  agg att ctg aag ctg aac tca act gaa tgg cct tat ttt gtg gtt ggt    2164
1828  Arg Ile Leu Lys Leu Asn Ser Thr Glu Trp Pro Tyr Phe Val Val Gly
1829                  705                 710                 715
1831  ata ttt tgt gct att ata aac gga ggc ctg caa cca gca ttt tca ata    2212
1832  Ile Phe Cys Ala Ile Ile Asn Gly Gly Leu Gln Pro Ala Phe Ser Ile
1833                  720                 725                 730
1835  ata ttt tca agg att ata ggg atc ttt acc cga gat gag gat cct gaa    2260
1836  Ile Phe Ser Arg Ile Ile Gly Ile Phe Thr Arg Asp Glu Asp Pro Glu
1837                  735                 740                 745
1839  aca aaa cga cag aat agt aac atg ttt tct gta ttg ttt cta gtc ctt    2308
1840  Thr Lys Arg Gln Asn Ser Asn Met Phe Ser Val Leu Phe Leu Val Leu
1841          750                 755                 760
1843  gga att att tct ttt att aca ttt ttc ctc cag ggc ttc aca ttt ggc    2356
1844  Gly Ile Ile Ser Phe Ile Thr Phe Phe Leu Gln Gly Phe Thr Phe Gly
1845  765                 770                 775                 780
1847  aaa gct ggg gag atc ctc act aag cgg ctt cga tac atg gtt ttc aga    2404
1848  Lys Ala Gly Glu Ile Leu Thr Lys Arg Leu Arg Tyr Met Val Phe Arg
1849                  785                 790                 795
1851  tcc atg ctg aga cag gat gtc agc tgg ttt gat gac cct aaa aac acc    2452
1852  Ser Met Leu Arg Gln Asp Val Ser Trp Phe Asp Asp Pro Lys Asn Thr
1853                  800                 805                 810
1855  act gga gca ttg aca acc agg ctt gcc aat gat gcg gct caa gtt aaa    2500
1856  Thr Gly Ala Leu Thr Thr Arg Leu Ala Asn Asp Ala Ala Gln Val Lys
1857          815                 820                 825
1859  ggg gct ata ggt tcc agg ctt gct gtc att acc cag aat ata gca aat    2548
1860  Gly Ala Ile Gly Ser Arg Leu Ala Val Ile Thr Gln Asn Ile Ala Asn
1861          830                 835                 840
1863  ctt ggg aca ggc att att ata tcc tta atc tat ggt tgg caa tta aca    2596
1864  Leu Gly Thr Gly Ile Ile Ile Ser Leu Ile Tyr Gly Trp Gln Leu Thr
1865  845                 850                 855                 860
1867  ctt tta ctc tta gca att gta ccc atc att gca ata gca gga gtt gtt    2644
1868  Leu Leu Leu Leu Ala Ile Val Pro Ile Ile Ala Ile Ala Gly Val Val
1869                  865                 870                 875
1871  gaa atg aaa atg ttg tct gga caa gca ctg aaa gat aag aaa gag cta    2692
1872  Glu Met Lys Met Leu Ser Gly Gln Ala Leu Lys Asp Lys Lys Glu Leu
1873                  880                 885                 890
1875  gaa gga gct ggg aag att gct aca gaa gcc atc gaa aac ttc cga act    2740
1876  Glu Gly Ala Gly Lys Ile Ala Thr Glu Ala Ile Glu Asn Phe Arg Thr
1877          895                 900                 905
1879  gtt gtt tct ttg act cgg gag cag aag ttt gaa tac atg tat gca cag    2788
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1880  Val Val Ser Leu Thr Arg Glu Gln Lys Phe Glu Tyr Met Tyr Ala Gln
1881      910             915                 920
1883  agt ttg caa gta cca tac aga aac tct ttg agg aaa gca cac atc ttc    2836
1884  Ser Leu Gln Val Pro Tyr Arg Asn Ser Leu Arg Lys Ala His Ile Phe
1885  925             930                 935                 940
1887  ggg gtc tca ttt tct atc acc cag gca atg atg tat ttt tcc tat gct    2884
1888  Gly Val Ser Phe Ser Ile Thr Gln Ala Met Met Tyr Phe Ser Tyr Ala
1889                  945                 950                 955
1891  ggc tgt ttc cgg ttt ggt gcc tac ttg gtg gca aat gag ttc atg aac    2932
1892  Gly Cys Phe Arg Phe Gly Ala Tyr Leu Val Ala Asn Glu Phe Met Asn
1893              960                 965                 970
1895  ttt cag gat gtt ctt ttg gta ttc tca gct att gtc ttt ggt gcc atg    2980
1896  Phe Gln Asp Val Leu Leu Val Phe Ser Ala Ile Val Phe Gly Ala Met
1897          975                 980                 985
1899  gca gtg ggg cag gtc agt tca ttt gct cct gac tat gcc aaa gcc aaa    3028
1900  Ala Val Gly Gln Val Ser Ser Phe Ala Pro Asp Tyr Ala Lys Ala Lys
1901      990                 995                 1000
1903  gta tca gca gcc cac gtc atc atg atc att gaa aaa agc cct ctg att    3076
1904  Val Ser Ala Ala His Val Ile Met Ile Ile Glu Lys Ser Pro Leu Ile
1905  1005                1010                1015                1020
1907  gac agc tac agc cct cac ggc ctc aag cca aat acg ttg gaa gga aat    3124
1908  Asp Ser Tyr Ser Pro His Gly Leu Lys Pro Asn Thr Leu Glu Gly Asn
1909                  1025                1030                1035
1911  gtg aca ttt aat gag gtc gtg ttc aac tat ccc act cga cca gac atc    3172
1912  Val Thr Phe Asn Glu Val Val Phe Asn Tyr Pro Thr Arg Pro Asp Ile
1913              1040                1045                1050
1915  ccc gtg ctc cag ggg ctg agc ctc gag gtg aag aag ggc cag acg ctg    3220
1916  Pro Val Leu Gln Gly Leu Ser Leu Glu Val Lys Lys Gly Gln Thr Leu
1917              1055                1060                1065
1919  gcc ctc gta ggt agc agt ggc tgt ggg aag agc aca gtt gtt cag ctc    3268
1920  Ala Leu Val Gly Ser Ser Gly Cys Gly Lys Ser Thr Val Val Gln Leu
1921      1070                1075                1080
1923  cta gag cgc ttc tat gac ccc ttg gct ggt tca gtg cta att gat ggc    3316
1924  Leu Glu Arg Phe Tyr Asp Pro Leu Ala Gly Ser Val Leu Ile Asp Gly
1925  1085                1090                1095                1100
1927  aaa gag ata aag cac ctg aat gtc cag tgg ctc cga gca cac ctg ggc    3364
1928  Lys Glu Ile Lys His Leu Asn Val Gln Trp Leu Arg Ala His Leu Gly
1929                  1105                1110                1115
1931  atc gtg tct cag gag ccc atc ctg ttt gac tgc agc att gcc gag aac    3412
1932  Ile Val Ser Gln Glu Pro Ile Leu Phe Asp Cys Ser Ile Ala Glu Asn
1933                  1120                1125                1130
1935  att gcc tat gga gac aac agc cgg gtc gta tca cat gaa gag att atg    3460
1936  Ile Ala Tyr Gly Asp Asn Ser Arg Val Val Ser His Glu Glu Ile Met
1937          1135                1140                1145
1939  cag gca gcc aag gag gcc aac ata cac cac ttc atc gag aca ctc cct    3508
1940  Gln Ala Ala Lys Glu Ala Asn Ile His His Phe Ile Glu Thr Leu Pro
1941      1150                1155                1160
1943  gag aaa tac aac acc aga gta gga gac aaa gga acc cag ctc tct ggt    3556
1944  Glu Lys Tyr Asn Thr Arg Val Gly Asp Lys Gly Thr Gln Leu Ser Gly
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                    RAW SEQUENCE LISTING              DATE: 10/06/2000
                    PATENT APPLICATION:  US/09/672,725    TIME: 12:46:04

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                    Output Set: N:\CRF3\10062000\I672725.raw

      1945  1165              1170              1175              1180
      1947  ggc cag aaa cag cgc att gcc ata gct cgc gct ctt gtt aga cag cct    3604
      1948  Gly Gln Lys Gln Arg Ile Ala Ile Ala Arg Ala Leu Val Arg Gln Pro
      1949                  1185              1190              1195
      1951  cat att ttg ctt ttg gat gaa gct aca tca gct ctg gat aca gaa agt    3652
      1952  His Ile Leu Leu Leu Asp Glu Ala Thr Ser Ala Leu Asp Thr Glu Ser
      1953                  1200              1205              1210
      1955  gaa aag gtt gtc caa gaa gcc ctg gac aaa gcc aga gaa ggc cgc acc    3700
      1956  Glu Lys Val Val Gln Glu Ala Leu Asp Lys Ala Arg Glu Gly Arg Thr
      1957          1215              1220              1225
      1959  tgc att gtg atc gcc cac cgc ttg tcc acc atc cag aat gca gat tta    3748
      1960  Cys Ile Val Ile Ala His Arg Leu Ser Thr Ile Gln Asn Ala Asp Leu
      1961      1230              1235              1240
      1963  ata gtg gtg ttt cag aat ggc aaa gtc aag gag cat ggc aca cat caa    3796
      1964  Ile Val Val Phe Gln Asn Gly Lys Val Lys Glu His Gly Thr His Gln
      1965  1245              1250              1255              1260
      1967  cag ctg ctg gcc cag aaa ggc atc tat ttt tcc atg gtc agt gtc cag    3844
      1968  Gln Leu Leu Ala Gln Lys Gly Ile Tyr Phe Ser Met Val Ser Val Gln
      1969              1265              1270              1275
      1971  gct gga gca aag cgc tagtgaactg tggccatatg agctgttaaa tattttttaa    3899
      1972  Ala Gly Ala Lys Arg
      1973              1280
      1975  tatttgtgtt aaaacatggc atttaatcaa agttaaaagg tgagcactta ctggaaaaac   3959
      1976  tatgtagaac tacctgttta acatttcttg ctgcaactga agatcattcc accaagttca   4019
      1977  gagtcttcag attttataat taaaggaacc aaaagaaaca ttatctgatg gaataaaata   4079
      1978  ctggtgttaa ttgcattata aaattataga gtaattcaaa gtagattttg ttaataaatt   4139
      1979  gtataatttt tgtttatatt ttatttgtaa cttactgctt tgctgaaaga ttatagaagt   4199
      1980  ggtaaaaagt actgaatgtt tgaataaagt gctagctata ataaaactaa actttatat    4259
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      2155  <213> ORGANISM: Canis familiaris
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      2159  <222> LOCATION: (17)...(3859)
      2161  <400> SEQUENCE: 24
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      2163                  Met Asp Pro Glu Gly Gly Arg Lys Gly Ser Ala Glu
      2164                   1               5                  10
      2166  aag aac ttc tgg aaa atg ggc aaa aaa agt aaa aaa aaa gag aag aaa     100
      2167  Lys Asn Phe Trp Lys Met Gly Lys Lys Ser Lys Lys Lys Glu Lys Lys
      2168          15              20              25
      2170  gaa aag aaa cca act gtc agc acg ttt gca atg ttt cgc tat tca aat     148
      2171  Glu Lys Lys Pro Thr Val Ser Thr Phe Ala Met Phe Arg Tyr Ser Asn
      2172          30              35              40
      2174  tgg ctt gat agg ttg tat atg ttg gtg ggg aca atg gct gcc atc atc     196
      2175  Trp Leu Asp Arg Leu Tyr Met Leu Val Gly Thr Met Ala Ala Ile Ile
      2176  45              50              55              60
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no end of line numbering. See p. 6

(4279)

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2178  cat gga gct gca ctc cct ctc atg atg ctg gtt ttt gga aac atg aca      244
2179  His Gly Ala Ala Leu Pro Leu Met Met Leu Val Phe Gly Asn Met Thr
2180               65                  70                  75
2182  gat agc ttt gca aat gca gga att tca aga aac aaa act ttt cca gtt      292
2183  Asp Ser Phe Ala Asn Ala Gly Ile Ser Arg Asn Lys Thr Phe Pro Val
2184               80                  85                  90
2186  ata att aat gaa agt att acg aac aat aca caa cat ttc atc aac cat      340
2187  Ile Ile Asn Glu Ser Ile Thr Asn Asn Thr Gln His Phe Ile Asn His
2188               95                 100                 105
2190  ctg gag gag gaa atg acc acg tat gcc tat tat tac agt ggg atc ggt      388
2191  Leu Glu Glu Glu Met Thr Thr Tyr Ala Tyr Tyr Tyr Ser Gly Ile Gly
2192          110                 115                 120
2194  gct ggc gtg ctg gtg gct gct tac atc cag gtt tca ttc tgg tgc ctg      436
2195  Ala Gly Val Leu Val Ala Ala Tyr Ile Gln Val Ser Phe Trp Cys Leu
2196  125                 130                 135                 140
2198  gca gca gga aga cag ata ctc aaa att aga aaa caa ttt ttt cat gct      484
2199  Ala Ala Gly Arg Gln Ile Leu Lys Ile Arg Lys Gln Phe Phe His Ala
2200                  145                 150                 155
2202  atc atg cga cag gag att ggc tgg ttt gac gtg cat gac gtt ggg gag      532
2203  Ile Met Arg Gln Glu Ile Gly Trp Phe Asp Val His Asp Val Gly Glu
2204              160                 165                 170
2206  ctt aac acc cgg ctc aca gac gat gtc tcc aaa atc aat gaa gga att      580
2207  Leu Asn Thr Arg Leu Thr Asp Asp Val Ser Lys Ile Asn Glu Gly Ile
2208              175                 180                 185
2210  ggc gac aaa att gga atg ttc ttt caa tca ata gca aca ttt ttc acc      628
2211  Gly Asp Lys Ile Gly Met Phe Phe Gln Ser Ile Ala Thr Phe Phe Thr
2212          190                 195                 200
2214  ggt ttt ata gtg ggg ttt aca cgt ggt tgg aag cta acc ctt gtg att      676
2215  Gly Phe Ile Val Gly Phe Thr Arg Gly Trp Lys Leu Thr Leu Val Ile
2216  205                 210                 215                 220
2218  ttg gcc atc agc cct gtt ctt gga ctt tca gcc gcc atc tgg gca aag      724
2219  Leu Ala Ile Ser Pro Val Leu Gly Leu Ser Ala Ala Ile Trp Ala Lys
2220                  225                 230                 235
2222  ata cta tct tca ttt act gat aaa gaa ctc ttg gcc tat gca aaa gct      772
2223  Ile Leu Ser Ser Phe Thr Asp Lys Glu Leu Leu Ala Tyr Ala Lys Ala
2224                  240                 245                 250
2226  gga gca gta gct gaa gaa gtc tta gca gca atc aga act gtg att gcc      820
2227  Gly Ala Val Ala Glu Glu Val Leu Ala Ala Ile Arg Thr Val Ile Ala
2228          255                 260                 265
2230  ttt gga gga caa aag aaa gaa ctt gaa agg tac aac aaa aat tta gaa      868
2231  Phe Gly Gly Gln Lys Lys Glu Leu Glu Arg Tyr Asn Lys Asn Leu Glu
2232          270                 275                 280
2234  gaa gct aaa gga att ggg ata aag aaa gct atc acg gcc aac att tct      916
2235  Glu Ala Lys Gly Ile Gly Ile Lys Lys Ala Ile Thr Ala Asn Ile Ser
2236  285                 290                 295                 300
2238  att ggt gcc gct ttc tta ttg atc tat gca tca tat gct ctg gct ttc      964
2239  Ile Gly Ala Ala Phe Leu Leu Ile Tyr Ala Ser Tyr Ala Leu Ala Phe
2240                  305                 310                 315
2242  tgg tat ggg acc tcc ttg gtc ctc tcc agt gaa tat tct att gga caa     1012
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RAW SEQUENCE LISTING                      DATE: 10/06/2000
PATENT APPLICATION:  US/09/672,725        TIME: 12:46:04

Input Set : A:\485402_1.txt
Output Set: N:\CRF3\10062000\I672725.raw

2243  Trp Tyr Gly Thr Ser Leu Val Leu Ser Ser Glu Tyr Ser Ile Gly Gln
2244          320                     325                 330
2246  gta ctc act gtc ttc ttt tct gta tta att ggg gct ttt agt att gga    1060
2247  Val Leu Thr Val Phe Phe Ser Val Leu Ile Gly Ala Phe Ser Ile Gly
2248          335                     340                 345
2250  cag gca tcc cca agc att gaa gca ttt gca aac gca aga gga gca gct    1108
2251  Gln Ala Ser Pro Ser Ile Glu Ala Phe Ala Asn Ala Arg Gly Ala Ala
2252          350                     355                 360
2254  tat gaa atc ttc aag ata att gac aat aaa cca agc att gac agc tat    1156
2255  Tyr Glu Ile Phe Lys Ile Ile Asp Asn Lys Pro Ser Ile Asp Ser Tyr
2256  365                     370                     375         380
2258  tcg aag agt gga cat aaa cca gat aat att aag gga aat ttg gaa ttc    1204
2259  Ser Lys Ser Gly His Lys Pro Asp Asn Ile Lys Gly Asn Leu Glu Phe
2260          .        385                     390                 395
2262  aaa aat gtt cac ttc agt tac cct tct cga aaa gaa gtt aag atc tta    1252
2263  Lys Asn Val His Phe Ser Tyr Pro Ser Arg Lys Glu Val Lys Ile Leu
2264          .        400                     405                 410
2266  aag ggt ctc aac ctg aag gtt cag agt ggg cag aca gtg gcg ctg gtt    1300
2267  Lys Gly Leu Asn Leu Lys Val Gln Ser Gly Gln Thr Val Ala Leu Val
2268          415                     420         .           425
2270  ggg aac agt ggc tgc ggg aag agc acg acc gtg cag ctg atg cag agg    1348
2271  Gly Asn Ser Gly Cys Gly Lys Ser Thr Thr Val Gln Leu Met Gln Arg
2272          430                     435                 440
2274  ctc tat gac ccc aca gat ggc atg gtc tgt att gat gga cag gac att    1396
2275  Leu Tyr Asp Pro Thr Asp Gly Met Val Cys Ile Asp Gly Gln Asp Ile
2276  445              .        450                 455             460
2278  agg acc ata aat gta agg cat ctt cgg gaa att act ggt gtg gtg agt    1444
2279  Arg Thr Ile Asn Val Arg His Leu Arg Glu Ile Thr Gly Val Val Ser
2280                  465                     470             475
2282  cag gag cct gtg ttg ttt gcc acc acg ata gct gaa aac att cgc tat    1492
2283  Gln Glu Pro Val Leu Phe Ala Thr Thr Ile Ala Glu Asn Ile Arg Tyr
2284              480                     485                 490
2286  ggc cgc gaa aat gtc acc atg gat gag att gag aaa gct gtt aag gaa    1540
2287  Gly Arg Glu Asn Val Thr Met Asp Glu Ile Glu Lys Ala Val Lys Glu
2288          .        495                     500         505
2290  gcc aat gcc tat gat ttt atc atg aaa cta cct aat aaa ttt gac act    1588
2291  Ala Asn Ala Tyr Asp Phe Ile Met Lys Leu Pro Asn Lys Phe Asp Thr
2292          510                     515                 520
2294  ctg gtt gga gag aga ggg gcc cag ctg agt ggt gga cag aaa cag aga    1636
2295  Leu Val Gly Glu Arg Gly Ala Gln Leu Ser Gly Gly Gln Lys Gln Arg
2296  525                     530                 535             540
2298  atc gcc att gct cgg gcc ctg gtt cgc aac ccc aag att ctt ctg ctg    1684
2299  Ile Ala Ile Ala Arg Ala Leu Val Arg Asn Pro Lys Ile Leu Leu Leu
2300                  545                     550                 555
2302  gat gag gca acg tca gct ctg gac act gaa agt gaa gca gtg gtt cag    1732
2303  Asp Glu Ala Thr Ser Ala Leu Asp Thr Glu Ser Glu Ala Val Val Gln
2304          .        560                     565                 570
2306  gtg gcc ctg gat aag gcc aga aaa ggc cgg act acc att gtg ata gct    1780
2307  Val Ala Leu Asp Lys Ala Arg Lys Gly Arg Thr Thr Ile Val Ile Ala
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2308          575              580              585
2310   cat cgt ttg tct aca gtt cgt aat gcc gat gtc att gct ggt ttt gat     1828
2311   His Arg Leu Ser Thr Val Arg Asn Ala Asp Val Ile Ala Gly Phe Asp
2312        590              595              600
2314   gat gga gtc att gtg gag aaa gga aat cat gat gaa ctc atg aaa gag     1876
2315   Asp Gly Val Ile Val Glu Lys Gly Asn His Asp Glu Leu Met Lys Glu
2316   605              610              615              620
2318   aag ggc att tac ttc aaa ctt gtc aca atg cag aca aga gga aat gaa     1924
2319   Lys Gly Ile Tyr Phe Lys Leu Val Thr Met Gln Thr Arg Gly Asn Glu
2320                625              630              635
2322   att gag tta gaa aat gcc act ggt gaa tcc aaa agt gaa agt gat gcc     1972
2323   Ile Glu Leu Glu Asn Ala Thr Gly Glu Ser Lys Ser Glu Ser Asp Ala
2324             640              645              650
2326   ttg gaa atg tct cca aaa gat tca ggg tcc agt tta ata aaa aga aga     2020
2327   Leu Glu Met Ser Pro Lys Asp Ser Gly Ser Ser Leu Ile Lys Arg Arg
2328        655              660              665
2330   tca act cgc agg agt ata cat gca cca caa ggc caa gac aga aag ctt     2068
2331   Ser Thr Arg Arg Ser Ile His Ala Pro Gln Gly Gln Asp Arg Lys Leu
2332        670              675              680
2334   ggt aca aaa gag gac ttg aat gag aat gta cct cca gtt tcc ttc tgg     2116
2335   Gly Thr Lys Glu Asp Leu Asn Glu Asn Val Pro Pro Val Ser Phe Trp
2336   685              690              695              700
2338   agg att ctg aag ctg aac tca act gaa tgg cct tat ttt gtg gtt ggt     2164
2339   Arg Ile Leu Lys Leu Asn Ser Thr Glu Trp Pro Tyr Phe Val Val Gly
2340             705              710              715
2342   ata ttt tgt gct att ata aac gga ggc ctg caa cca gca ttt tca ata     2212
2343   Ile Phe Cys Ala Ile Ile Asn Gly Gly Leu Gln Pro Ala Phe Ser Ile
2344             720              725              730
2346   ata ttt tca agg att ata ggg atc ttt acc cga gat gag gat cct gaa     2260
2347   Ile Phe Ser Arg Ile Ile Gly Ile Phe Thr Arg Asp Glu Asp Pro Glu
2348             735              740              745
2350   aca aaa cga cag aat agt aac atg ttt tct gta ttg ttt cta gtc ctt     2308
2351   Thr Lys Arg Gln Asn Ser Asn Met Phe Ser Val Leu Phe Leu Val Leu
2352        750              755              760
2354   gga att att tct ttt att aca ttt ttc ctc cag ggc ttc aca ttt ggc     2356
2355   Gly Ile Ile Ser Phe Ile Thr Phe Phe Leu Gln Gly Phe Thr Phe Gly
2356   765              770              775              780
2358   aaa gct ggg gag atc ctc act aag cgg ctt cga tac atg gtt ttc aga     2404
2359   Lys Ala Gly Glu Ile Leu Thr Lys Arg Leu Arg Tyr Met Val Phe Arg
2360             785              790              795
2362   tcc atg ctg aga cag gat gtc agc tgg ttt gat gac cct aaa aac acc     2452
2363   Ser Met Leu Arg Gln Asp Val Ser Trp Phe Asp Asp Pro Lys Asn Thr
2364             800              805              810
2366   act gga gca ttg aca acc agg ctt gcc aat gat gcg gct caa gtt aaa     2500
2367   Thr Gly Ala Leu Thr Thr Arg Leu Ala Asn Asp Ala Ala Gln Val Lys
2368        815              820              825
2370   ggg gct ata ggt tcc agg ctt gct gtc att acc cag aat ata gca aat     2548
2371   Gly Ala Ile Gly Ser Arg Leu Ala Val Ile Thr Gln Asn Ile Ala Asn
2372        830              835              840
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2374  ctt ggg aca ggc att att ata tcc tta atc tat ggt tgg caa tta aca   2596
2375  Leu Gly Thr Gly Ile Ile Ile Ser Leu Ile Tyr Gly Trp Gln Leu Thr
2376  845                     850                 855             860
2378  ctt tta ctc tta gca att gta ccc atc att gca ata gca gga gtt gtt   2644
2379  Leu Leu Leu Leu Ala Ile Val Pro Ile Ile Ala Ile Ala Gly Val Val
2380                  865                 870                 875
2382  gaa atg aaa atg ttg tct gga caa gca ctg aaa gat aag aaa gag cta   2692
2383  Glu Met Lys Met Leu Ser Gly Gln Ala Leu Lys Asp Lys Lys Glu Leu
2384              880                 885                 890
2386  gaa gga gct ggg aag att gct aca gaa gcc atc gaa aac ttc cga act   2740
2387  Glu Gly Ala Gly Lys Ile Ala Thr Glu Ala Ile Glu Asn Phe Arg Thr
2388          895                 900                 905
2390  gtt gtt tct ttg act cgg gag cag aag ttt gaa tac atg tat gca cag   2788
2391  Val Val Ser Leu Thr Arg Glu Gln Lys Phe Glu Tyr Met Tyr Ala Gln
2392          910                 915                 920
2394  agt ttg caa gta cca tac aga aac tct ttg agg aaa gca cac atc ttc   2836
2395  Ser Leu Gln Val Pro Tyr Arg Asn Ser Leu Arg Lys Ala His Ile Phe
2396  925                 930                 935                 940
2398  ggg gtc tca ttt tct atc acc cag gca atg atg tat ttt tcc tat gct   2884
2399  Gly Val Ser Phe Ser Ile Thr Gln Ala Met Met Tyr Phe Ser Tyr Ala
2400                  945                 950                 955
2402  ggc tgt ttc cgg ttt ggt gcc tac ttg gtg gca aat gag ttc atg aac   2932
2403  Gly Cys Phe Arg Phe Gly Ala Tyr Leu Val Ala Asn Glu Phe Met Asn
2404              960                 965                 970
2406  ttt cag gat gtt ctt ttg gta ttc tca gct att gtc ttt ggt gcc atg   2980
2407  Phe Gln Asp Val Leu Leu Val Phe Ser Ala Ile Val Phe Gly Ala Met
2408          975                 980                 985
2410  gca gtg ggg cag gtc agt tca ttt gct cct gac tat gcc aaa gcc aaa   3028
2411  Ala Val Gly Gln Val Ser Ser Phe Ala Pro Asp Tyr Ala Lys Ala Lys
2412          990                 995                 1000
2414  gta tca gca gcc cac gtc atc atg atc att gaa aaa agc cct ctg att   3076
2415  Val Ser Ala Ala His Val Ile Met Ile Ile Glu Lys Ser Pro Leu Ile
2416  1005                1010                1015                1020
2418  gac agc tac agc cct cac ggc ctc aag cca aat acg ttg gaa gga aat   3124
2419  Asp Ser Tyr Ser Pro His Gly Leu Lys Pro Asn Thr Leu Glu Gly Asn
2420              1025                1030                1035
2422  gtg aca ttt aat gag gtc gtg ttc aac tat ccc act cga cca gac atc   3172
2423  Val Thr Phe Asn Glu Val Val Phe Asn Tyr Pro Thr Arg Pro Asp Ile
2424              1040                1045                1050
2426  ccc gtg ctc cag ggg ctg agc ctc gag gtg aag aag ggc cag acg ctg   3220
2427  Pro Val Leu Gln Gly Leu Ser Leu Glu Val Lys Lys Gly Gln Thr Leu
2428          1055                1060                1065
2430  gcc ctc gta ggt agc agt ggc tgt ggg aag agc aca gtt gtt cag ctc   3268
2431  Ala Leu Val Gly Ser Ser Gly Cys Gly Lys Ser Thr Val Val Gln Leu
2432      1070                1075                1080
2434  cta gag cgc ttc tat gac ccc ttg gct ggt tca gtg cta att gat ggc   3316
2435  Leu Glu Arg Phe Tyr Asp Pro Leu Ala Gly Ser Val Leu Ile Asp Gly
2436  1085                1090                1095                1100
2438  aaa gag ata aag cac ctg aat gtc cag tgg ctc cga gca cac ctg ggc   3364
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2439    Lys Glu Ile Lys His Leu Asn Val Gln Trp Leu Arg Ala His Leu Gly
2440              1105                1110                1115
2442    atc gtg tct cag gag ccc atc ctg ttt gac tgc agc att gcc gag aac      3412
2443    Ile Val Ser Gln Glu Pro Ile Leu Phe Asp Cys Ser Ile Ala Glu Asn
2444              1120                1125                1130
2446    att gcc tat gga gac aac agc cgg gtc gta tca cat gaa gag att atg      3460
2447    Ile Ala Tyr Gly Asp Asn Ser Arg Val Val Ser His Glu Glu Ile Met
2448              1135                1140                1145
2450    cag gca gcc aag gag gcc aac ata cac cac ttc atc gag aca ctc cct      3508
2451    Gln Ala Ala Lys Glu Ala Asn Ile His His Phe Ile Glu Thr Leu Pro
2452              1150                1155                1160
2454    gag aaa tac aac acc aga gta gga gac aaa gga acc cag ctc tct ggt      3556
2455    Glu Lys Tyr Asn Thr Arg Val Gly Asp Lys Gly Thr Gln Leu Ser Gly
2456    1165                1170                1175                1180
2458    ggc cag aaa cag cgc att gcc ata gct cgc gct ctt gtt aga cag cct      3604
2459    Gly Gln Lys Gln Arg Ile Ala Ile Ala Arg Ala Leu Val Arg Gln Pro
2460              1185                1190                1195
2462    cat att ttg ctt ttg gat gaa gct aca tca gct ctg gat aca gaa agt      3652
2463    His Ile Leu Leu Leu Asp Glu Ala Thr Ser Ala Leu Asp Thr Glu Ser
2464              1200                1205                1210
2466    gaa aag gtt gtc caa gaa gcc ctg gac aaa gcc aga gaa ggc cgc acc      3700
2467    Glu Lys Val Val Gln Glu Ala Leu Asp Lys Ala Arg Glu Gly Arg Thr
2468              1215                1220                1225
2470    tgc att gtg atc gcc cac cgc ttg tcc acc atc cag aat gca gat tta      3748
2471    Cys Ile Val Ile Ala His Arg Leu Ser Thr Ile Gln Asn Ala Asp Leu
2472       1230                1235                1240
2474    ata gtg gtg ttt cag aat ggc aaa gtc aag gag cat ggc aca cat caa      3796
2475    Ile Val Val Phe Gln Asn Gly Lys Val Lys Glu His Gly Thr His Gln
2476    1245                1250                1255                1260
2478    cag ctg ctg gcc cag aaa ggc atc tat ttt tcc atg gtc agt gtc cag      3844
2479    Gln Leu Leu Ala Gln Lys Gly Ile Tyr Phe Ser Met Val Ser Val Gln
2480              1265                1270                1275
2482    gct gga gca aag cgc tagtgaactg tggccatatg agctgttaaa tattttttaa      3899
2483    Ala Gly Ala Lys Arg
2484              1280
2486    tatttgtgtt aaaacatggc atttaatcaa agttaaaagg tgagcactta ctggaaaaac    3959
2487    tatgtagaac tacctgttta acatttcttg ctgcaactga agatcattcc accaagttca    4019
2488    gagtcttcag attttataat taaggaacc aaaagaaaca ttatctgatg gaataaaata     4079
2489    ctggtgttaa ttgcattata aaattataga gtaattcaaa gtagattttg ttaataaatt    4139
2490    gtataatttt tgtttatatt ttatttgtaa cttactgctt tgctgaaaga ttatagaagt    4199
2491    ggtaaaaagt actgaatgtt tgaataaagt gctagctata ataaaactaa acttttatat    4259
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2666    <213> ORGANISM: Canis familiaris
2668    <220> FEATURE:
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2670    <222> LOCATION: (17)...(3859)
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(4279) refer to p.6

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2672  <400> SEQUENCE: 26
2673  ggagcgcgag gtcggg atg gat cct gaa gga ggc cgt aag ggg agt gca gag      52
2674                     Met Asp Pro Glu Gly Gly Arg Lys Gly Ser Ala Glu
2675                      1               5                  10
2677  aag aac ttc tgg aaa atg ggc aaa aaa agt aaa aaa aaa gag aag aaa       100
2678  Lys Asn Phe Trp Lys Met Gly Lys Lys Ser Lys Lys Lys Glu Lys Lys
2679               15                  20                  25
2681  gaa aag aaa cca act gtc agc acg ttt gca atg ttt cgc tat tca aat      148
2682  Glu Lys Lys Pro Thr Val Ser Thr Phe Ala Met Phe Arg Tyr Ser Asn
2683        30                  35                  40
2685  tgg ctt gat agg ttg tat atg ttg gtg ggg aca atg gct gcc atc atc      196
2686  Trp Leu Asp Arg Leu Tyr Met Leu Val Gly Thr Met Ala Ala Ile Ile
2687   45                  50                  55                  60
2689  cat gga gct gca ctc cct ctc atg atg ctg gtt ttt gga aac atg aca      244
2690  His Gly Ala Ala Leu Pro Leu Met Met Leu Val Phe Gly Asn Met Thr
2691                   65                  70                  75
2693  gat agc ttt gca aat gca gga att tca aga aac aaa act ttt cca gtt      292
2694  Asp Ser Phe Ala Asn Ala Gly Ile Ser Arg Asn Lys Thr Phe Pro Val
2695               80                  85                  90
2697  ata att aat gaa agt att acg aac aat aca caa cat ttc atc aac cat      340
2698  Ile Ile Asn Glu Ser Ile Thr Asn Asn Thr Gln His Phe Ile Asn His
2699               95                 100                 105
2701  ctg gag gag gaa atg acc acg tat gcc tat tat tac agt ggg atc ggt      388
2702  Leu Glu Glu Glu Met Thr Thr Tyr Ala Tyr Tyr Tyr Ser Gly Ile Gly
2703       110                 115                 120
2705  gct ggc gtg ctg gtg gct gct tac atc cag gtt tca ttc tgg tgc ctg      436
2706  Ala Gly Val Leu Val Ala Ala Tyr Ile Gln Val Ser Phe Trp Cys Leu
2707  125                 130                 135                 140
2709  gca gca gga aga cag ata ctc aaa att aga aaa caa ttt ttt cat gct      484
2710  Ala Ala Gly Arg Gln Ile Leu Lys Ile Arg Lys Gln Phe Phe His Ala
2711               145                 150                 155
2713  atc atg cga cag gag att ggc tgg ttt gac gtg cat gac gtt ggg gag      532
2714  Ile Met Arg Gln Glu Ile Gly Trp Phe Asp Val His Asp Val Gly Glu
2715               160                 165                 170
2717  ctt aac acc cgg ctc aca gac gat gtc tcc aaa atc aat gaa gga att      580
2718  Leu Asn Thr Arg Leu Thr Asp Asp Val Ser Lys Ile Asn Glu Gly Ile
2719               175                 180                 185
2721  ggc gac aaa att gga atg ttc ttt caa tca ata gca aca ttt ttc acc      628
2722  Gly Asp Lys Ile Gly Met Phe Phe Gln Ser Ile Ala Thr Phe Phe Thr
2723       190                 195                 200
2725  ggt ttt ata gtg ggg ttt aca cgt ggt tgg aag cta acc ctt gtg att      676
2726  Gly Phe Ile Val Gly Phe Thr Arg Gly Trp Lys Leu Thr Leu Val Ile
2727  205                 210                 215                 220
2729  .ttg gcc atc agc cct gtt ctt gga ctt tca gcc gcc atc tgg gca aag     724
2730  Leu Ala Ile Ser Pro Val Leu Gly Leu Ser Ala Ala Ile Trp Ala Lys
2731                   225                 230                 235
2733  ata cta tct tca ttt act gat aaa gaa ctc ttg gcc tat gca aaa gct      772
2734  Ile Leu Ser Ser Phe Thr Asp Lys Glu Leu Leu Ala Tyr Ala Lys Ala
2735               240                 245                 250
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2737   gga gca gta gct gaa gaa gtc tta gca gca atc aga act gtg att gcc        820
2738   Gly Ala Val Ala Glu Glu Val Leu Ala Ala Ile Arg Thr Val Ile Ala
2739           255                 260                 265
2741   ttt gga gga caa aag aaa gaa ctt gaa agg tac aac aaa aat tta gaa        868
2742   Phe Gly Gly Gln Lys Lys Glu Leu Glu Arg Tyr Asn Lys Asn Leu Glu
2743           270                 275                 280
2745   gaa gct aaa gga att ggg ata aag aaa gct atc acg gcc aac att tct        916
2746   Glu Ala Lys Gly Ile Gly Ile Lys Lys Ala Ile Thr Ala Asn Ile Ser
2747   285                 290                 295                 300
2749   att ggt gcc gct ttc tta ttg atc tat gca tca tat gct ctg gct ttc        964
2750   Ile Gly Ala Ala Phe Leu Leu Ile Tyr Ala Ser Tyr Ala Leu Ala Phe
2751                   305                 310                 315
2753   tgg tat ggg acc tcc ttg gtc ctc tcc agt gaa tat act att gga caa       1012
2754   Trp Tyr Gly Thr Ser Leu Val Leu Ser Ser Glu Tyr Thr Ile Gly Gln
2755                   320                 325                 330
2757   gta ctc act gtc ttc ttt tct gta tta att ggg gct ttt agt att gga       1060
2758   Val Leu Thr Val Phe Phe Ser Val Leu Ile Gly Ala Phe Ser Ile Gly
2759               335                 340                 345
2761   cag gca tcc cca agc att gaa gca ttt gca aac gca aga gga gca gct       1108
2762   Gln Ala Ser Pro Ser Ile Glu Ala Phe Ala Asn Ala Arg Gly Ala Ala
2763           350                 355                 360
2765   tat gaa atc ttc aag ata att gac aat aaa cca agc att gac agc tat       1156
2766   Tyr Glu Ile Phe Lys Ile Ile Asp Asn Lys Pro Ser Ile Asp Ser Tyr
2767   365                 370                 375                 380
2769   tcg aag agt gga cat aaa cca gat aat att aag gga aat ttg gaa ttc       1204
2770   Ser Lys Ser Gly His Lys Pro Asp Asn Ile Lys Gly Asn Leu Glu Phe
2771                   385                 390                 395
2773   aaa aat gtt cac ttc agt tac cct tct cga aaa gaa gtt aag atc tta       1252
2774   Lys Asn Val His Phe Ser Tyr Pro Ser Arg Lys Glu Val Lys Ile Leu
2775                   400                 405                 410
2777   aag ggt ctc aac ctg aag gtt cag agt ggg cag aca gtg gcg ctg gtt       1300
2778   Lys Gly Leu Asn Leu Lys Val Gln Ser Gly Gln Thr Val Ala Leu Val
2779               415                 420                 425
2781   ggg aac agt ggc tgc ggg aag agc acg acc gtg cag ctg atg cag agg       1348
2782   Gly Asn Ser Gly Cys Gly Lys Ser Thr Thr Val Gln Leu Met Gln Arg
2783           430                 435                 440
2785   ctc tat gac ccc aca gat ggc atg gtc tgt att gat gga cag gac att       1396
2786   Leu Tyr Asp Pro Thr Asp Gly Met Val Cys Ile Asp Gly Gln Asp Ile
2787   445                 450                 455                 460
2789   agg acc ata aat gta agg cat ctt cgg gaa att act ggt gtg gtg agt       1444
2790   Arg Thr Ile Asn Val Arg His Leu Arg Glu Ile Thr Gly Val Val Ser
2791                   465                 470                 475
2793   cag gag cct gtg ttg ttt gcc acc acg ata gct gaa aac att cgc tat       1492
2794   Gln Glu Pro Val Leu Phe Ala Thr Thr Ile Ala Glu Asn Ile Arg Tyr
2795                   480                 485                 490
2797   ggc cgc gaa aat gtc acc atg gat gag att gag aaa gct gtt aag gaa       1540
2798   Gly Arg Glu Asn Val Thr Met Asp Glu Ile Glu Lys Ala Val Lys Glu
2799               495                 500                 505
2801   gcc aat gcc tat gat ttt atc atg aaa cta cct aat aaa ttt gac act       1588
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2802  Ala Asn Ala Tyr Asp Phe Ile Met Lys Leu Pro Asn Lys Phe Asp Thr
2803          510                 515                 520
2805  ctg gtt gga gag aga ggg gcc cag ctg agt ggt gga cag aaa cag aga    1636
2806  Leu Val Gly Glu Arg Gly Ala Gln Leu Ser Gly Gly Gln Lys Gln Arg
2807  525                 530                 535                 540
2809  atc gcc att gct cgg gcc ctg gtt cgc aac ccc aag att ctt ctg ctg    1684
2810  Ile Ala Ile Ala Arg Ala Leu Val Arg Asn Pro Lys Ile Leu Leu Leu
2811                      545                 550                 555
2813  gat gag gca acg tca gct ctg gac act gaa agt gaa gca gtg gtt cag    1732
2814  Asp Glu Ala Thr Ser Ala Leu Asp Thr Glu Ser Glu Ala Val Val Gln
2815                      560                 565                 570
2817  gtg gcc ctg gat aag gcc aga aaa ggc cgg act acc att gtg ata gct    1780
2818  Val Ala Leu Asp Lys Ala Arg Lys Gly Arg Thr Thr Ile Val Ile Ala
2819          575                 580                 585
2821  cat cgt ttg tct aca gtt cgt aat gcc gat gtc att gct ggt ttt gat    1828
2822  His Arg Leu Ser Thr Val Arg Asn Ala Asp Val Ile Ala Gly Phe Asp
2823          590                 595                 600
2825  gat gga gtc att gtg gag aaa gga aat cat gat gaa ctc atg aaa gag    1876
2826  Asp Gly Val Ile Val Glu Lys Gly Asn His Asp Glu Leu Met Lys Glu
2827  605                 610                 615                 620
2829  aag ggc att tac ttc aaa ctt gtc aca atg cag aca aga gga aat gaa    1924
2830  Lys Gly Ile Tyr Phe Lys Leu Val Thr Met Gln Thr Arg Gly Asn Glu
2831                      625                 630                 635
2833  att gag tta gaa aat gcc act ggt gaa tcc aaa agt gaa agt gat gcc    1972
2834  Ile Glu Leu Glu Asn Ala Thr Gly Glu Ser Lys Ser Glu Ser Asp Ala
2835              640                 645                 650
2837  ttg gaa atg tct cca aaa gat tca ggg tcc agt tta ata aaa aga aga    2020
2838  Leu Glu Met Ser Pro Lys Asp Ser Gly Ser Ser Leu Ile Lys Arg Arg
2839          655                 660                 665
2841  tca act cgc agg agt ata cat gca cca caa ggc caa gac aga aag ctt    2068
2842  Ser Thr Arg Arg Ser Ile His Ala Pro Gln Gly Gln Asp Arg Lys Leu
2843          670                 675                 680
2845  ggt aca aaa gag gac ttg aat gag aat gta cct cca gtt tcc ttc tgg    2116
2846  Gly Thr Lys Glu Asp Leu Asn Glu Asn Val Pro Pro Val Ser Phe Trp
2847  685                 690                 695                 700
2849  agg att ctg aag ctg aac tca act gaa tgg cct tat ttt gtg gtt ggt    2164
2850  Arg Ile Leu Lys Leu Asn Ser Thr Glu Trp Pro Tyr Phe Val Val Gly
2851                      705                 710                 715
2853  ata ttt tgt gct att ata aac gga ggc ctg caa cca gca ttt tca ata    2212
2854  Ile Phe Cys Ala Ile Ile Asn Gly Gly Leu Gln Pro Ala Phe Ser Ile
2855              720                 725                 730
2857  ata ttt tca agg att ata ggg atc ttt acc cga gat gag gat cct gaa    2260
2858  Ile Phe Ser Arg Ile Ile Gly Ile Phe Thr Arg Asp Glu Asp Pro Glu
2859          735                 740                 745
2861  aca aaa cga cag aat agt aac atg ttt tct gta ttg ttt cta gtc ctt    2308
2862  Thr Lys Arg Gln Asn Ser Asn Met Phe Ser Val Leu Phe Leu Val Leu
2863          750                 755                 760
2865  gga att att tct ttt att aca ttt ttc ctc cag ggc ttc aca ttt ggc    2356
2866  Gly Ile Ile Ser Phe Ile Thr Phe Phe Leu Gln Gly Phe Thr Phe Gly
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2867  765                 770                 775                 780
2869  aaa gct ggg gag atc ctc act aag cgg ctt cga tac atg gtt ttc aga      2404
2870  Lys Ala Gly Glu Ile Leu Thr Lys Arg Leu Arg Tyr Met Val Phe Arg
2871                  785                 790                 795
2873  tcc atg ctg aga cag gat gtc agc tgg ttt gat gac cct aaa aac acc      2452
2874  Ser Met Leu Arg Gln Asp Val Ser Trp Phe Asp Asp Pro Lys Asn Thr
2875                  800                 805                 810
2877  act gga gca ttg aca acc agg ctt gcc aat gat gcg gct caa gtt aaa      2500
2878  Thr Gly Ala Leu Thr Thr Arg Leu Ala Asn Asp Ala Ala Gln Val Lys
2879          815                 820                 825
2881  ggg gct ata ggt tcc agg ctt gct gtc att acc cag aat ata gca aat      2548
2882  Gly Ala Ile Gly Ser Arg Leu Ala Val Ile Thr Gln Asn Ile Ala Asn
2883          830                 835                 840
2885  ctt ggg aca ggc att att ata tcc tta atc tat ggt tgg caa tta aca      2596
2886  Leu Gly Thr Gly Ile Ile Ile Ser Leu Ile Tyr Gly Trp Gln Leu Thr
2887  845                 850                 855                 860
2889  ctt tta ctc tta gca att gta ccc atc att gca ata gca gga gtt gtt      2644
2890  Leu Leu Leu Leu Ala Ile Val Pro Ile Ile Ala Ile Ala Gly Val Val
2891                  865                 870                 875
2893  gaa atg aaa atg ttg tct gga caa gca ctg aaa gat aag aaa gag cta      2692
2894  Glu Met Lys Met Leu Ser Gly Gln Ala Leu Lys Asp Lys Lys Glu Leu
2895                  880                 885                 890
2897  gaa gga gct ggg aag att gct aca gaa gcc atc gaa aac ttc cga act      2740
2898  Glu Gly Ala Gly Lys Ile Ala Thr Glu Ala Ile Glu Asn Phe Arg Thr
2899          895                 900                 905
2901  gtt gtt tct ttg act cgg gag cag aag ttt gaa tac atg tat gca cag      2788
2902  Val Val Ser Leu Thr Arg Glu Gln Lys Phe Glu Tyr Met Tyr Ala Gln
2903          910                 915                 920
2905  agt ttg caa gta cca tac aga aac tct ttg agg aaa gca cac atc ttc      2836
2906  Ser Leu Gln Val Pro Tyr Arg Asn Ser Leu Arg Lys Ala His Ile Phe
2907  925                 930                 935                 940
2909  ggg gtc tca ttt tct atc acc cag gca atg atg tat ttt tcc tat gct      2884
2910  Gly Val Ser Phe Ser Ile Thr Gln Ala Met Met Tyr Phe Ser Tyr Ala
2911                  945                 950                 955
2913  ggc tgt ttc cgg ttt ggt gcc tac ttg gtg gca aat gag ttc atg aac      2932
2914  Gly Cys Phe Arg Phe Gly Ala Tyr Leu Val Ala Asn Glu Phe Met Asn
2915                  960                 965                 970
2917  ttt cag gat gtt ctt ttg gta ttc tca gct att gtc ttt ggt gcc atg      2980
2918  Phe Gln Asp Val Leu Leu Val Phe Ser Ala Ile Val Phe Gly Ala Met
2919                  975                 980                 985
2921  gca gtg ggg cag gtc agt tca ttt gct cct gac tat gcc aaa gcc aaa      3028
2922  Ala Val Gly Gln Val Ser Ser Phe Ala Pro Asp Tyr Ala Lys Ala Lys
2923          990                 995                 1000
2925  gta tca gca gcc cac gtc atc atg atc att gaa aaa agc cct ctg att      3076
2926  Val Ser Ala Ala His Val Ile Met Ile Ile Glu Lys Ser Pro Leu Ile
2927  1005                1010                1015                1020
2929  gac agc tac agc cct cac ggc ctc aag cca aat acg ttg gaa gga aat      3124
2930  Asp Ser Tyr Ser Pro His Gly Leu Lys Pro Asn Thr Leu Glu Gly Asn
2931                  1025                1030                1035
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2933  gtg aca ttt aat gag gtc gtg ttc aac tat ccc act cga cca gac atc       3172
2934  Val Thr Phe Asn Glu Val Val Phe Asn Tyr Pro Thr Arg Pro Asp Ile
2935            1040                    1045                    1050
2937  ccc gtg ctc cag ggg ctg agc ctc gag gtg aag aag ggc cag acg ctg       3220
2938  Pro Val Leu Gln Gly Leu Ser Leu Glu Val Lys Lys Gly Gln Thr Leu
2939            1055                    1060                    1065
2941  gcc ctc gta ggt agc agt ggc tgt ggg aag agc aca gtt gtt cag ctc       3268
2942  Ala Leu Val Gly Ser Ser Gly Cys Gly Lys Ser Thr Val Val Gln Leu
2943        1070                    1075                    1080
2945  cta gag cgc ttc tat gac ccc ttg gct ggt tca gtg cta att gat ggc       3316
2946  Leu Glu Arg Phe Tyr Asp Pro Leu Ala Gly Ser Val Leu Ile Asp Gly
2947  1085                    1090                    1095                1100
2949  aaa gag ata aag cac ctg aat gtc cag tgg ctc cga gca cac ctg ggc       3364
2950  Lys Glu Ile Lys His Leu Asn Val Gln Trp Leu Arg Ala His Leu Gly
2951            1105                    1110                    1115
2953  atc gtg tct cag gag ccc atc ctg ttt gac tgc agc att gcc gag aac       3412
2954  Ile Val Ser Gln Glu Pro Ile Leu Phe Asp Cys Ser Ile Ala Glu Asn
2955            1120                    1125                    1130
2957  att gcc tat gga gac aac agc cgg gtc gta tca cat gaa gag att gtg       3460
2958  Ile Ala Tyr Gly Asp Asn Ser Arg Val Val Ser His Glu Glu Ile Val
2959            1135                    1140                    1145
2961  cag gca gcc aag gag gcc aac ata cac cac ttc atc gag aca ctc cct       3508
2962  Gln Ala Ala Lys Glu Ala Asn Ile His His Phe Ile Glu Thr Leu Pro
2963        1150                    1155                    1160
2965  gag aaa tac aac acc aga gta gga gac aaa gga acc cag ctc tct ggt       3556
2966  Glu Lys Tyr Asn Thr Arg Val Gly Asp Lys Gly Thr Gln Leu Ser Gly
2967  1165                    1170                    1175                1180
2969  ggc cag aaa cag cgc att gcc ata gct cgc gct ctt gtt aga cag cct       3604
2970  Gly Gln Lys Gln Arg Ile Ala Ile Ala Arg Ala Leu Val Arg Gln Pro
2971                1185                    1190                    1195
2973  cat att ttg ctt ttg gat gaa gct aca tca gct ctg gat aca gaa agt       3652
2974  His Ile Leu Leu Leu Asp Glu Ala Thr Ser Ala Leu Asp Thr Glu Ser
2975            1200                    1205                    1210
2977  gaa aag gtt gtc caa gaa gcc ctg gac aaa gcc aga gaa ggc cgc acc       3700
2978  Glu Lys Val Val Gln Glu Ala Leu Asp Lys Ala Arg Glu Gly Arg Thr
2979        1215                    1220                    1225
2981  tgc att gtg atc gcc cac cgc ttg tcc acc atc cag aat gca gat tta       3748
2982  Cys Ile Val Ile Ala His Arg Leu Ser Thr Ile Gln Asn Ala Asp Leu
2983        1230                    1235                    1240
2985  ata gtg gtg ttt cag aat ggc aaa gtc aag gag cat ggc aca cat caa       3796
2986  Ile Val Phe Gln Asn Gly Lys Val Lys Glu His Gly Thr His Gln
2987  1245                    1250                    1255                1260
2989  cag ctg ctg gcc cag aaa ggc atc tat ttt tcc atg gtc agt gtc cag       3844
2990  Gln Leu Leu Ala Gln Lys Gly Ile Tyr Phe Ser Met Val Ser Val Gln
2991            1265                    1270                    1275
2993  gct gga gca aag cgc tagtgaactg tggccatatg agctgttaaa tattttttaa       3899
2994  Ala Gly Ala Lys Arg
2995            1280
2997  tatttgtgtt aaaacatggc atttaatcaa agttaaaagg tgagcactta ctggaaaaac    3959
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  2998  tatgtagaac tacctgttta acatttcttg ctgcaactga agatcattcc accaagttca  4019
  2999  gagtcttcag attttataat taaaggaacc aaaagaaaca ttatctgatg gaataaaata  4079
  3000  ctggtgttaa ttgcattata aaattataga gtaattcaaa gtagattttg ttaataaatt  4139
  3001  gtataatttt tgtttatatt ttatttgtaa cttactgctt tgctgaaaga ttatagaagt  4199
  3002  ggtaaaaagt actgaatgtt tgaataaagt gctagctata ataaaactaa acttttatat  4259
E--> 3003  caaaaaaaaa aaaaaaaaaa                                                4279
```

(4279) refer to p.6

<210> 28   Seq # 28
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 28
nntttttttt tttttttttt tttttttttt ttcgccggcg acttaagatc tt   52

missing mandatory <220> to <223> features to explain "n's" in sequence. See #10 on Error Summary Sheet.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/672,725   DATE: 10/06/2000
                                        TIME: 12:46:06

Input Set : A:\485402_1.txt
Output Set: N:\CRF3\10062000\I672725.raw

L:15 M:270 C: Current Application Number differs, Replaced Current Application No
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:362 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:362 M:252 E: No. of Seq. differs, <211>LENGTH:Input:4279 Found:4259 SEQ:1
L:499 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:874 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:4317 SEQ:3
L:1981 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:1981 M:252 E: No. of Seq. differs, <211>LENGTH:Input:4279 Found:4259 SEQ:22
L:2492 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:2492 M:252 E: No. of Seq. differs, <211>LENGTH:Input:4279 Found:4259 SEQ:24
L:3003 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:3003 M:252 E: No. of Seq. differs, <211>LENGTH:Input:4279 Found:4259 SEQ:26
L:3183 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:28
L:3183 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:28
L:3183 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:28